

SEQUENCE LISTING

<110> Rosson, Reinhardt D.
Deng, Ming-de
Grund, Alan D.

<120> LINOLEATE ISOMERASE

<130> 3161-20-C1

<140> Not Yet Assigned

<141> 2000-04-28

<150> 60/141,798

<151> 1999-06-30

<160> 80

<170> PatentIn Ver. 2.1

<210> 1

<211> 35

<212> PRT

<213> Lactobacillus reuteri

<220>

<221> UNSURE

<222> (30)

<223> Xaa = any amino acid

<400> 1

Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Xaa Gly Leu
20 25 30

Ala Ser Leu
35

<210> 2

<211> 29

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> unsure

<222> (1)..(29)

<223> n = a, c, g, or t

<400> 2

cgtgaattca tgtaytayws naayggnaa

29

<210> 3

<211> 27

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> unsure
<222> (1)..(27)
<223> n = a, c, g, or t

<400> 3
actggatccn acdatratng crtgytt

27

<210> 4
<211> 87
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (1)..(87)

<400> 4
atg tat tat tcg aac gga aat tat gaa gcc ttt gct cga cca aag aag 48
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

cct gct ggc gtt gat aag aaa cac gcc tac ata gtc gga 87
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly
20 25

<210> 5
<211> 29
<212> PRT
<213> Lactobacillus reuteri

<400> 5
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly
20 25

<210> 6
<211> 17
<212> DNA
<213> Lactobacillus reuteri

<400> 6
ggtcgagcaa aggcttc 17

<210> 7
<211> 17
<212> DNA
<213> Lactobacillus reuteri

<400> 7
aagcctgctg gcgttga 17

<210> 8
<211> 596

<212> DNA
<213> Lactobacillus reuteri

<220>
<221> CDS
<222> (122)..(595)

<400> 8
aaaaattatt tagaattaat ttataagttc attgtgttta ataaaattga cacttttcaac 60
cgcttttcaact aaaattaagg tagttatgat gcacttgttt actgagaagg gagtcgtcaa 120

a atg tat tat tca aac ggg aat tat gaa gcc ttt gct cga cca aag aag 169
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

cct gct ggc gtt gat aag aaa cat gcc tac att gtc ggt ggt ggt tta 217
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu
20 25 30

gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg 265
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
35 40 45

ggt gag aat atc cat att tta gag gaa tta ccg gtt gcc ggt ggt tct 313
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
50 55 60

ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc 361
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
65 70 75 80

cgg gaa atg gag aac cat ttc gag tgt atg tgg gac atg tat cgt tca 409
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
85 90 95

att cca tca ctt gaa atc cca ggt gct tcc tac ctt gat gaa tac tac 457
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
100 105 110

tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat 505
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
115 120 125

aag cgg gga aat gaa gtt cca tcg gac ggt aaa tat ggt tta agt aaa 553
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
130 135 140

aag gca atc aaa gag ctg act aag cta att atg acc cct aaa g 596
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Lys
145 150 155

<210> 9
<211> 158
<212> PRT
<213> Lactobacillus reuteri

<400> 9
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
1 5 10 15

Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu
 20 25 30
 Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
 35 40 45
 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95
 Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110
 Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125
 Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
 130 135 140
 Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Lys
 145 150 155

<210> 10

<211> 1709

<212> DNA

<213> *Lactobacillus reuteri*

<400> 10

cggaaggcat	caaaatccca	atgaattccc	accaaactta	gtgcataggg	caagaagggt	60
gtcccgcgat	tggtatgcat	ggattggaac	ccgcctttaa	gattaatgcg	cctgaaggaa	120
gccagctggt	cgccaatccg	tagcaccatt	ccctgggcaa	ttcggctttt	atattgaccg	180
agttgtcctg	ttaaccagg	catcaccttg	ccacgccctt	ccttgacggg	caagatgatt	240
tacagcatag	ggtgcacttg	caatccttagc	gttaagattt	gtttggttat	tattgataat	300
aaacgcaccg	gctttgttcc	aggtaattga	aatgccaaagt	tgttggcgaa	cagccggagt	360
taagactgaa	ttagcctggt	cctgagttgg	cggtaatggt	tttttgatcg	ttgtgactgg	420
ttttcttcca	ataagcaatt	ttactaatat	ggtttaacga	agcatttggt	agctgagggt	480
gctggataac	tccagtaact	actaataaac	cagcaagagc	aaataaaaagg	tgatagaggc	540
gtttcttaag	tttcataaat	tactccatt	tctaataatt	ccaaagtcta	ttttactagt	600
ttgaacatac	gtttggaata	attatttaga	attaatttat	aagttcattg	tgtttaataa	660
aattgacact	ttcaaccgct	ttcactaaaa	ttaaggtagt	tatgatgcac	ttgtttactg	720
agaagggagt	cgtcaaaatg	tattattcaa	acgggaatta	tgaagccttt	gctcgaccaa	780
agaagcctgc	tggcgttgat	aagaaacatg	cctacattgt	cggtgggtgt	ttagctggtt	840
tatcggccgc	cgtgttttta	attcgtgatg	cccaaagtc	gggtgagaat	atccatattt	900
tagaggaatt	accggttgcc	ggtggttctc	ttgatgggga	agatcgctct	ggaattggtt	960
ttgttactcg	tggaggccgg	gaaatggaga	accatttcga	gtgtatgtgg	gacatgtatc	1020
gttcaattcc	atcacttgaa	atcccagggtg	cttcctacct	tgatgaatac	tactgggttag	1080
ataaggaaga	tccaaacagt	tctaattgtc	gtttaaccta	taagcgggga	aatgaagttc	1140
catcggacgg	taaatatggt	ttaagtaaaa	aggcaatcaa	agagctgact	aagctaatta	1200
tgacccttga	agaaaaattg	ggaagggaga	ctattgggtga	atacttctct	gatgatttct	1260
ttgaaagcaa	tttctggatt	tattgggtcaa	caatgtttgc	gtttgaacgg	tggcactctc	1320
tagctgaaat	gcgtcggtat	atgatgcggt	ttattcacca	tattgatggt	ttaccggatt	1380
tcactgcact	gaagtttaat	aagtataacc	aatatgaatc	aatgaccaag	ccgctattgg	1440
cctacctgaa	agatcatcat	gtcaagattg	agtacgatac	ccaggtaaag	aatgttattg	1500

ttgataactca tgggcggcaa aagcacgcta agcgaatctt attaaactcaa gccggtaaag 1560
 ataaagttgt tgagttaacg gacaatgacc ttgtctttgt cacaaacggt tcaattacag 1620
 aaagttctac ttacggcagt caccatcaag ccagctcgac caacgcagca cttggtgggt 1680
 agttggaaac tgtgggaaaa ccttgctcc 1709

<210> 11
 <211> 324
 <212> PRT
 <213> Lactobacillus reuteri

<220>
 <221> UNSURE
 <222> (315)
 <223> Xaa = any amino acid

<400> 11
 Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys
 1 5 10 15
 Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu
 20 25 30
 Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro
 35 40 45
 Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser
 50 55 60
 Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly
 65 70 75 80
 Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser
 85 90 95
 Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr
 100 105 110
 Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr
 115 120 125
 Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys
 130 135 140
 Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys
 145 150 155 160
 Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu
 165 170 175
 Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp
 180 185 190
 His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His
 195 200 205
 Ile Asp Gly Leu Pro Asp Phe Thr Ala Leu Lys Phe Asn Lys Tyr Asn
 210 215 220
 Gln Tyr Glu Ser Met Thr Lys Pro Leu Leu Ala Tyr Leu Lys Asp His
 225 230 235 240

His Val Lys Ile Glu Tyr Asp Thr Gln Val Lys Asn Val Ile Val Asp
 245 250 255

Thr His Gly Arg Gln Lys His Ala Lys Arg Ile Leu Leu Thr Gln Ala
 260 265 270

Gly Lys Asp Lys Val Val Glu Leu Thr Asp Asn Asp Leu Val Phe Val
 275 280 285

Thr Asn Gly Ser Ile Thr Glu Ser Ser Thr Tyr Gly Ser His His Gln
 290 295 300

Ala Ser Ser Thr Asn Ala Ala Leu Gly Gly Xaa Leu Glu Thr Val Gly
 305 310 315 320

Lys Pro Cys Ser

<210> 12
 <211> 17
 <212> DNA
 <213> Lactobacillus reuteri

<400> 12
 ccaattccag gacgatc

17

<210> 13
 <211> 19
 <212> DNA
 <213> Lactobacillus reuteri

<400> 13
 acatgtatcg ttcaattcc

19

<210> 14
 <211> 1165
 <212> DNA
 <213> Lactobacillus reuteri

<400> 14
 aagcctgctg gcgttgataa gaaacatgcc tacattgtcg gtggtggttt agctgggttta 60
 tcggccgccc tggttttaatt tccgtgatgcc caaatgccgg gtgagaatat ccatatttta 120
 gaggaattac cgggtgaata attaatgga atgtttcttt ggacattcgg aacaaagaca 180
 ttgtattcta gagaaccatc actagattta gcttcgatat gagcacctgc cggaacgata 240
 ttattaccgt cataaatatt ggtaactcgg tagcgaactt gcttattctg atctaagtct 300
 tttctcacca gaccttcgta gtaattttgc cctgttgagt tcttacttcg tgcttcattt 360
 gccagggcag tttgcgtggc aatattagat ggatttgatt cggatgcatc aaatccatga 420
 ataccacca actagtgcac agggcaagaa ggtgtccgcg atcgtatgca tgattgtacc 480
 cgcctttaag attatgcgcc tgaaaggaag ccagctggtc gccaatccgt agcaccattc 540
 cctgggcaat tcggctttta tattgaccga gttgtcctgt ttaaccaggc atcaccttgc 600
 cagcccttc cttgacggtc aagatgattt acagcatagg gtgcacttgc aatcttagcg 660
 ttaagatttg tttggttatt attgataata aacgcaccgg ctttgttcca ggtaattgaa 720
 atgccaaagt gttggcgaac agccggagtt aagactgaat tagcctgttc ctgagttggc 780
 ggtaattggt ttttgatcgt tgtgactggt tttcttccaa taagcaattt tactaatatg 840
 gtttaacgaa gcatttggtta gctgaggttg ctggataact ccagtaacta ctaataaacc 900
 agcaagagca aataaaaggat gatagaggcg tttcttaagt ttcataaatt cactccattt 960
 ctaataattc caaagtctat tttactagtt tgaacatacg tttggaataa ttatttagaa 1020

ttaatttata agttcattgt gtttaataaa attgacactt tcaaccgctt tcaactaaaat 1080
 taaggtagtt atgatgcact tgtttactga gaagggagtc gtcaaaatgt attattcaaa 1140
 cgggaattat gaagcctttg ctcga 1165

<210> 15
 <211> 2319
 <212> DNA
 <213> *Lactobacillus reuteri*

<400> 15
 ccaattccag gacgatcttc accatcaaga gaaccaccgg caaccgggtcc cttaccgcta 60
 tctgatctt tctttccttc ctcaacttgc ttttgagctg cctttactag gttcatagta 120
 aagaagggt tcaatactgg cttaaaatcc tttttaaagt ggtagtaag gttttggtat 180
 aagcggacat cattgtcaaa taccaatact tcttcaaatt gatttcggtg agcatcaaat 240
 gaagcttcgt ctaaactctac actcccaaga atcacacggg aatcatgagt agttgaacta 300
 cttaacaagt aaaacttaga atggataacc tgagtaggag cgattgatac gcgaaaaaga 360
 ttatttaaga cgttcgtttg gttgtcactg gttaacgctg agaagagttt agcagcttct 420
 ttatttgctg aactaaggag agcattggta gctacattaa tactgataaa attactaagg 540
 cttaattcac tagttgattg ggagcttaac agtgcaacct ttgtcaccat ctcatcagca 480
 tattttattaa tgaagtcagc agtaattttc ccagttactg cgattaactg atcgtatttt 600
 tgtgaatcaa ataattgatg gatctttaat ggtggtgttt cttgaccatc aaaaacaata 660
 tgaatttttc ttataccagc agtttctgtc atgaccataa tcctttacta tcaataaata 720
 tattagtttt attttcgact atttaatccc tttttgcaag tggttccccg ataagctata 780
 taaaaaaga agccggaaat ttccagcttc ttcatcttt atagtaagtg ctgttgctcc 840
 attaattcac caatccacgt tccttgaggt ttctttaata atggcttttc aacaatcttt 900
 ggaattggca agtccatgtc ttttaacggc ttcttatcat tcatgtaata cattgcccgc 960
 attaactctc gaagatcata aatagagtta aagacttctg gaactccccg atcaacatct 1020
 aatagagtgt agacggcttc cattgcggtc cgtactgaat attccgtggt aaatacggta 1080
 tctcgacttg gagattcagc aaagttaacca ataaatgcc aagtagcgga tccttctgga 1140
 acaacgtctg gacggtcgcc cttaactcgt ggcataaagt agctagtgat aaatggcata 1200
 tatactggaa cagtattaat tgaactctcc ttagccaaat cgtcaattaa cggttctggt 1260
 aacccccaga tggatagcca ttcttttagta atctcttcac cagtacaatc aacgatccgt 1320
 ttcttaatat agtttccctt tgtattagag tacagaccgt aaatccaaac aatggtttca 1380
 tttttctttt gtttcttgaa gtgcggttga cgggtgaattg tccaggaaag catccaatta 1440
 gagtcagtga ccgtaaatgat tccaccagta ttaactttgc catcatggag atctcgcttg 1500
 gttaagcggt caatgtatgg ttcaacttgc gggttcttaa cggttgcagt agcggaaatg 1560
 aaccagcttc tccctggaag attcttgcaa aagacatcag gatgaccaa atcagctgac 1620
 tgccgagcaa ggttttccca cagtttccaa ctaccaccaa gtgctgcgtt ggtcgagctg 1680
 cttgatggtg actgccgtaa gtagaacttt ctgtaattga accgtttgtg acaaagacaa 1740
 ggtcattgtc cgtaactca acaactttat ctttaccggc ttgagttaat aagattcgct 1800
 tagcgtgctt ttgcccgcct tgagtatcaa caataacatt ctttacctgg gtatcgact 1860
 caatcttgac atgatgact ttccagtagg ccaatagcgg cttgggtcatt gattcatatt 1920
 ggttatactt attaaacttc agtgcagtga aatccggtta accatcaata tgggaataa 1980
 accgcatcat ataacgagc atttcagcta gagagtgcc cggttcaaac gcaaacattg 2040
 ttgaccaata aatccagaaa ttgctttcaa agaaatcatc agagaagtat tcaccaatag 2100
 tctcccttcc caatttttct tcaggggtca taattagctt agtcagctct ttgattgcct 2160
 ttttacttaa accatattta ccgtccgatg gaacttcatt tccccgctta taggttaaac 2220
 gacaattaga actgtttgga tottccctat ctaaccagta gtattcatca aggtaggaag 2280
 cacctgggat ttcaagtgat ggaattgaac gatacatgt 2319

<210> 16
 <211> 3551
 <212> DNA
 <213> *Lactobacillus reuteri*

<400> 16
 accggttgaa taattaatgg taatgtttct ttggacattc ggaacaaaga cattgtattc 60
 tagagaacca tcaactagatt tagcttcgat atgagcacct gccggaacga tattattacc 120
 gtcataaata ttggtaactc ggtagcgaac ttgcttattc tgatctaag cttttctcac 180

cagaccttcg	tagtaatttt	gccctgttga	gttcttactt	cgtgcttcat	ttgccaggc	240
agtttgctg	gcaatattag	atggatttga	ttcggatgca	tcaaattccat	gaataccacc	300
aactagtgc	taggcaagaa	ggtgtccg	atcgtatgca	tgattgtacc	cgcctttaag	360
attatgcgc	tgaaaggaag	ccagctggc	gccaatccgt	agcaccattc	cctgtggcaa	420
atttcggctt	ttatattgac	cgagttgtcc	tgtttaacca	ggcatcacct	tgccacgccc	480
ttccttgacg	gtcaagatga	tttacagcat	agggtgcact	tgcaatctta	gcgttaagat	540
ttgtttggtt	attattgata	ataaacgcac	cggctttggt	ccaggttaatt	gaaatgccaa	600
gttggtggcg	aacagccgga	gttaagactg	aattagcctg	ttcctgagtt	ggcggtaatg	660
tttttttgat	cggtgtgact	ggttttcttc	caataagcaa	ttttactaat	atgggttaac	720
gaagcatttg	ttagctgagg	ttgctggata	actccagtaa	ctactaataa	accagcaaga	780
gcaaataaaa	ggtgatagag	gcgtttctta	agtttcataa	attcactcca	tttctaataa	840
ttccaaagtc	tattttacta	gtttgaacat	acgtttggaa	taattattta	gaattaattt	900
ataagttcat	tgtgtttaat	aaaattgaca	ctttcaaccg	ctttcactaa	aattaaggta	960
gttatgatgc	acttggttac	tgagaaggga	gtcgtcaaaa	tgtattattc	aaacgggaat	1020
tatgaagcct	ttgctcgacc	aaagaagcct	gctggcggtg	ataagaaaca	tgccacatt	1080
gtcgggtggtg	gttttagctgg	tttatcggcc	gccgtgtttt	taattcgtga	tgcccaaatg	1140
ccgggtgaga	atatccatat	tttagaggaa	ttaccgggtg	ccgggtggtt	tcttgatggt	1200
gaagatcgtc	ctggaattgg	ttttgttact	cgtggaggcc	gggaaatgga	gaaccatttc	1260
gagtgatgtg	gggacatgta	tcgttcaatt	ccatcacttg	aaatcccagg	tgcttccctac	1320
cttgatgaat	actactgggt	agataaggaa	gatccaaaca	gttctaattg	tcgtttaacc	1380
tataagcggg	gaaatgaagt	tccatcggac	ggtaaatatg	gtttaagtaa	aaaggcaatc	1440
aaagagctga	ctaagcta	tatgacccct	gaagaaaaat	tggaaggga	gactattggt	1500
gaatacttct	ctgatgattt	ctttgaaagc	aatttctgga	tttattgggt	aacaatgttt	1560
gcgtttgaac	ggtggcactc	tctagctgaa	atgcgtcggt	atatgatgcg	gtttattcac	1620
catattgatg	gtttaccgga	tttactgca	ctgaagttta	ataagtataa	ccaatatgaa	1680
tcaatgacca	agccgctatt	ggcctacctg	aaagatcatc	atgtcaagat	tgagtacgat	1740
accaggttaa	agaatgttat	tggtgatact	catggcgccg	aaaagcacgc	taagcgaatc	1800
ttattaactc	aagccggtaa	agataaagtt	gttgagttaa	cggacaatga	ccttgtcttt	1860
gtcacaacacg	gttcaattac	agaaaagttc	acttacggca	gtcaccatca	agcagctcga	1920
ccaacgcaag	cacttggtgg	tagttggaaa	ctgtgggaaa	accttgctcg	gcagtcagct	1980
gattttgggtc	atcctgatgt	cttttgcaag	aatcttccag	ggagaagctg	gttcatttcc	2040
gctactgcaa	ccgttaagaa	cccgaagtt	gaaccataca	ttgaacgctt	aaccaagcga	2100
gatctccatg	atggcaaagt	taatactggt	ggaatcatta	cggtcactga	ctctaattgg	2160
atgctttcct	ggacaattca	ccgtcaaccg	cacttcaaga	aacaaaagaa	aatgaaacc	2220
attgttttga	tttacgggtc	gtactcta	acaaaggga	actatattaa	gaaacggatc	2280
gttgattgta	ctgggtgaaga	gattactaaa	gaatggctat	ccatctgggg	gttccagaag	2340
ccgttaattg	acgatttggc	taaggagagt	tcaattaata	ctgttccagt	atatatgcca	2400
tttatcacta	gctactttat	gccacgagtt	aagggcgacc	gtccagacgt	tggtccagaa	2460
ggatccgcta	acttggcatt	tattggtaac	tttgcgtaat	ctccaagtcg	agataccgta	2520
tttaccacgg	aatattcagt	acggaccgca	atggaagccg	tctacactct	attagatggt	2580
gatcggggag	ttccagaagt	ctttaactct	atztatgatc	ttcgagagtt	aatgcgggca	2640
atgtattata	tgaatgataa	gaagccgtta	aaagacatgg	acttgccaat	tccaaagatt	2700
gttgaaaagc	cattattaaa	gaaactccaa	ggaacgtgga	ttggtgaatt	aatggagcaa	2760
cagcacttac	tataaagatg	aaagaagctg	gaaatttccg	gcttcttttt	ttatatagct	2820
tatcggggaa	ccacttgcaa	aaagggatta	aatagtcgaa	aataaaaacta	atatatttat	2880
tgatagtaaa	ggattatggt	catgacagaa	actgctggta	taagaaaaat	tcatattggt	2940
tttgatgggtc	aagaaacacc	accattaaaag	atccatcaat	tatttgattc	acaaaaatac	3000
gatcagttaa	tcgcagtaac	tgggaaaatt	actgctgact	tcattaataa	ataccttagt	3060
aattttatca	gtattaatgt	agcgttaagc	tcccaatcaa	ctagtgaatt	aagtgcgtgat	3120
gagatgggtga	caaagggtgc	acttaccat	gctctcctta	gttcagcaaa	taaagaagct	3180
gctaaactct	tctcagcggt	aaccagtgac	aaccaaacga	acgtcttaaa	taatcttttt	3240
cgcgtatcaa	tcgcgcctac	tcaggttata	cattctaagt	tttacttggt	aagtgttca	3300
actactcatg	attcccgtgt	gattcttggg	agtgtagatt	tagacgaagc	ttcatttgat	3360
gctcaccgaa	atcaatttga	agaagtattg	gtatttgaca	atgatgtccg	cttatacca	3420
aaccttactg	accactttaa	aaaggatttt	aagccagtat	tgaagccctt	ctttactatg	3480
aacctagtaa	aggcagctca	aaagcaagtt	gaggaaggaa	agaaagatca	ggatagcggg	3540
aagggaccgg	t					3551

<210> 17
<211> 1776

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> CDS

<222> (1)..(1776)

<400> 17

atg tat tat tca aac ggg aat tat gaa gcc ttt gct cga cca aag aag	48
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys	
1 5 10 15	
cct gct ggc gtt gat aag aaa cat gcc tac att gtc ggt ggt ggt tta	96
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Gly Leu	
20 25 30	
gct ggt tta tcg gcc gcc gtg ttt tta att cgt gat gcc caa atg ccg	144
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro	
35 40 45	
ggt gag aat atc cat att tta gag gaa tta ccg gtt gcc ggt ggt tct	192
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser	
50 55 60	
ctt gat ggt gaa gat cgt cct gga att ggt ttt gtt act cgt gga ggc	240
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly	
65 70 75 80	
cgg gaa atg gag aac cat ttc gag tgt atg tgg gac atg tat cgt tca	288
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser	
85 90 95	
att cca tca ctt gaa atc cca ggt gct tcc tac ctt gat gaa tac tac	336
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr	
100 105 110	
tgg tta gat aag gaa gat cca aac agt tct aat tgt cgt tta acc tat	384
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr	
115 120 125	
aag cgg gga aat gaa gtt cca tcg gac ggt aaa tat ggt tta agt aaa	432
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys	
130 135 140	
aag gca atc aaa gag ctg act aag cta att atg acc cct gaa gaa aaa	480
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys	
145 150 155 160	
ttg gga agg gag act att ggt gaa tac ttc tct gat gat ttc ttt gaa	528
Leu Gly Arg Glu Thr Ile Gly Glu Tyr Phe Ser Asp Asp Phe Phe Glu	
165 170 175	
agc aat ttc tgg att tat tgg tca aca atg ttt gcg ttt gaa cgg tgg	576
Ser Asn Phe Trp Ile Tyr Trp Ser Thr Met Phe Ala Phe Glu Arg Trp	
180 185 190	
cac tct cta gct gaa atg cgt cgt tat atg atg cgg ttt att cac cat	624
His Ser Leu Ala Glu Met Arg Arg Tyr Met Met Arg Phe Ile His His	
195 200 205	
att gat ggt tta ccg gat ttc act gca ctg aag ttt aat aag tat aac	672

Ile	Asp	Gly	Leu	Pro	Asp	Phe	Thr	Ala	Leu	Lys	Phe	Asn	Lys	Tyr	Asn		
210						215					220						
caa	tat	gaa	tca	atg	acc	aag	ccg	cta	ttg	gcc	tac	ctg	aaa	gat	cat	720	
Gln	Tyr	Glu	Ser	Met	Thr	Lys	Pro	Leu	Leu	Ala	Tyr	Leu	Lys	Asp	His		
225					230					235					240		
cat	gtc	aag	att	gag	tac	gat	acc	cag	gta	aag	aat	gtt	att	gtt	gat	768	
His	Val	Lys	Ile	Glu	Tyr	Asp	Thr	Gln	Val	Lys	Asn	Val	Ile	Val	Asp		
				245					250					255			
act	cat	ggg	cgg	caa	aag	cac	gct	aag	cga	atc	tta	tta	act	caa	gcc	816	
Thr	His	Gly	Arg	Gln	Lys	His	Ala	Lys	Arg	Ile	Leu	Leu	Thr	Gln	Ala		
			260					265					270				
ggt	aaa	gat	aaa	gtt	gtt	gag	tta	acg	gac	aat	gac	ctt	gtc	ttt	gtc	864	
Gly	Lys	Asp	Lys	Val	Val	Glu	Leu	Thr	Asp	Asn	Asp	Leu	Val	Phe	Val		
		275					280					285					
aca	aac	ggt	tca	att	aca	gaa	agt	tct	act	tac	ggc	agt	cac	cat	caa	912	
Thr	Asn	Gly	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Tyr	Gly	Ser	His	His	Gln		
	290					295					300						
gca	gct	cga	cca	acg	caa	gca	ctt	ggt	ggt	agt	tgg	aaa	ctg	tgg	gaa	960	
Ala	Ala	Arg	Pro	Thr	Gln	Ala	Leu	Gly	Gly	Ser	Trp	Lys	Leu	Trp	Glu		
305					310					315					320		
aac	ctt	gct	cgg	cag	tca	gct	gat	ttt	ggt	cat	cct	gat	gtc	ttt	tgc	1008	
Asn	Leu	Ala	Arg	Gln	Ser	Ala	Asp	Phe	Gly	His	Pro	Asp	Val	Phe	Cys		
				325					330					335			
aag	aat	ctt	cca	ggg	aga	agc	tgg	ttc	att	tcc	gct	act	gca	acc	gtt	1056	
Lys	Asn	Leu	Pro	Gly	Arg	Ser	Trp	Phe	Ile	Ser	Ala	Thr	Ala	Thr	Val		
			340					345					350				
aag	aac	ccg	caa	gtt	gaa	cca	tac	att	gaa	cgc	tta	acc	aag	cga	gat	1104	
Lys	Asn	Pro	Gln	Val	Glu	Pro	Tyr	Ile	Glu	Arg	Leu	Thr	Lys	Arg	Asp		
		355					360					365					
ctc	cat	gat	ggc	aaa	gtt	aat	act	ggt	gga	atc	att	acg	gtc	act	gac	1152	
Leu	His	Asp	Gly	Lys	Val	Asn	Thr	Gly	Gly	Ile	Ile	Thr	Val	Thr	Asp		
	370					375					380						
tct	aat	tgg	atg	ctt	tcc	tgg	aca	att	cac	cgt	caa	ccg	cac	ttc	aag	1200	
Ser	Asn	Trp	Met	Leu	Ser	Trp	Thr	Ile	His	Arg	Gln	Pro	His	Phe	Lys		
385					390					395					400		
aaa	caa	aag	aaa	aat	gaa	acc	att	gtt	tgg	att	tac	ggt	ctg	tac	tct	1248	
Lys	Gln	Lys	Lys	Asn	Glu	Thr	Ile	Val	Trp	Ile	Tyr	Gly	Leu	Tyr	Ser		
				405					410					415			
aat	aca	aag	gga	aac	tat	att	aag	aaa	cgg	atc	gtt	gat	tgt	act	ggt	1296	
Asn	Thr	Lys	Gly	Asn	Tyr	Ile	Lys	Lys	Arg	Ile	Val	Asp	Cys	Thr	Gly		
			420					425					430				
gaa	gag	att	act	aaa	gaa	tgg	cta	tcc	atc	tgg	ggg	ttc	cag	aag	ccg	1344	
Glu	Glu	Ile	Thr	Lys	Glu	Trp	Leu	Ser	Ile	Trp	Gly	Phe	Gln	Lys	Pro		
		435					440					445					
tta	att	gac	gat	ttg	gct	aag	gag	agt	tca	att	aat	act	gtt	cca	gta	1392	
Leu	Ile	Asp	Asp	Leu	Ala	Lys	Glu	Ser	Ser	Ile	Asn	Thr	Val	Pro	Val		

450	455	460	
tat atg cca ttt atc act agc tac ttt atg cca cga gtt aag ggc gac			1440
Tyr Met Pro Phe Ile Thr Ser Tyr Phe Met Pro Arg Val Lys Gly Asp			
465	470	475	480
cgt cca gac gtt gtt cca gaa gga tcc gct aac ttg gca ttt att ggt			1488
Arg Pro Asp Val Val Pro Glu Gly Ser Ala Asn Leu Ala Phe Ile Gly			
	485	490	495
aac ttt gct gaa tct cca agt cga gat acc gta ttt acc acg gaa tat			1536
Asn Phe Ala Glu Ser Pro Ser Arg Asp Thr Val Phe Thr Thr Glu Tyr			
	500	505	510
tca gta cgg acc gca atg gaa gcc gtc tac act cta tta gat gtt gat			1584
Ser Val Arg Thr Ala Met Glu Ala Val Tyr Thr Leu Leu Asp Val Asp			
	515	520	525
cgg gga gtt cca gaa gtc ttt aac tct att tat gat ctt cga gag tta			1632
Arg Gly Val Pro Glu Val Phe Asn Ser Ile Tyr Asp Leu Arg Glu Leu			
	530	535	540
atg cgg gca atg tat tac atg aat gat aag aag ccg tta aaa gac atg			1680
Met Arg Ala Met Tyr Tyr Met Asn Asp Lys Lys Pro Leu Lys Asp Met			
	545	550	555
gac ttg cca att cca aag att gtt gaa aag cca tta tta aag aaa ctc			1728
Asp Leu Pro Ile Pro Lys Ile Val Glu Lys Pro Leu Leu Lys Lys Leu			
	565	570	575
caa gga acg tgg att ggt gaa tta atg gag caa cag cac tta cta taa			1776
Gln Gly Thr Trp Ile Gly Glu Leu Met Glu Gln Gln His Leu Leu			
	580	585	590

<210> 18
 <211> 591
 <212> PRT
 <213> Lactobacillus reuteri

<400> 18	
Met Tyr Tyr Ser Asn Gly Asn Tyr Glu Ala Phe Ala Arg Pro Lys Lys	
1 5 10 15	
Pro Ala Gly Val Asp Lys Lys His Ala Tyr Ile Val Gly Gly Leu	
20 25 30	
Ala Gly Leu Ser Ala Ala Val Phe Leu Ile Arg Asp Ala Gln Met Pro	
35 40 45	
Gly Glu Asn Ile His Ile Leu Glu Glu Leu Pro Val Ala Gly Gly Ser	
50 55 60	
Leu Asp Gly Glu Asp Arg Pro Gly Ile Gly Phe Val Thr Arg Gly Gly	
65 70 75 80	
Arg Glu Met Glu Asn His Phe Glu Cys Met Trp Asp Met Tyr Arg Ser	
85 90 95	
Ile Pro Ser Leu Glu Ile Pro Gly Ala Ser Tyr Leu Asp Glu Tyr Tyr	
100 105 110	
Trp Leu Asp Lys Glu Asp Pro Asn Ser Ser Asn Cys Arg Leu Thr Tyr	
115 120 125	
Lys Arg Gly Asn Glu Val Pro Ser Asp Gly Lys Tyr Gly Leu Ser Lys	
130 135 140	
Lys Ala Ile Lys Glu Leu Thr Lys Leu Ile Met Thr Pro Glu Glu Lys	
145 150 155 160	

Leu	Gly	Arg	Glu	Thr	Ile	Gly	Glu	Tyr	Phe	Ser	Asp	Asp	Phe	Phe	Glu	
				165					170						175	
Ser	Asn	Phe	Trp	Ile	Tyr	Trp	Ser	Thr	Met	Phe	Ala	Phe	Glu	Arg	Trp	
			180					185					190			
His	Ser	Leu	Ala	Glu	Met	Arg	Arg	Tyr	Met	Met	Arg	Phe	Ile	His	His	
		195					200					205				
Ile	Asp	Gly	Leu	Pro	Asp	Phe	Thr	Ala	Leu	Lys	Phe	Asn	Lys	Tyr	Asn	
	210					215					220					
Gln	Tyr	Glu	Ser	Met	Thr	Lys	Pro	Leu	Leu	Ala	Tyr	Leu	Lys	Asp	His	
225					230					235					240	
His	Val	Lys	Ile	Glu	Tyr	Asp	Thr	Gln	Val	Lys	Asn	Val	Ile	Val	Asp	
				245					250					255		
Thr	His	Gly	Arg	Gln	Lys	His	Ala	Lys	Arg	Ile	Leu	Leu	Thr	Gln	Ala	
		260						265					270			
Gly	Lys	Asp	Lys	Val	Val	Glu	Leu	Thr	Asp	Asn	Asp	Leu	Val	Phe	Val	
	275						280					285				
Thr	Asn	Gly	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Tyr	Gly	Ser	His	His	Gln	
	290					295					300					
Ala	Ala	Arg	Pro	Thr	Gln	Ala	Leu	Gly	Gly	Ser	Trp	Lys	Leu	Trp	Glu	
305					310					315					320	
Asn	Leu	Ala	Arg	Gln	Ser	Ala	Asp	Phe	Gly	His	Pro	Asp	Val	Phe	Cys	
				325					330					335		
Lys	Asn	Leu	Pro	Gly	Arg	Ser	Trp	Phe	Ile	Ser	Ala	Thr	Ala	Thr	Val	
		340						345					350			
Lys	Asn	Pro	Gln	Val	Glu	Pro	Tyr	Ile	Glu	Arg	Leu	Thr	Lys	Arg	Asp	
	355						360					365				
Leu	His	Asp	Gly	Lys	Val	Asn	Thr	Gly	Gly	Ile	Ile	Thr	Val	Thr	Asp	
	370					375					380					
Ser	Asn	Trp	Met	Leu	Ser	Trp	Thr	Ile	His	Arg	Gln	Pro	His	Phe	Lys	
385					390					395					400	
Lys	Gln	Lys	Lys	Asn	Glu	Thr	Ile	Val	Trp	Ile	Tyr	Gly	Leu	Tyr	Ser	
				405					410					415		
Asn	Thr	Lys	Gly	Asn	Tyr	Ile	Lys	Lys	Arg	Ile	Val	Asp	Cys	Thr	Gly	
		420						425					430			
Glu	Glu	Ile	Thr	Lys	Glu	Trp	Leu	Ser	Ile	Trp	Gly	Phe	Gln	Lys	Pro	
	435						440					445				
Leu	Ile	Asp	Asp	Leu	Ala	Lys	Glu	Ser	Ser	Ile	Asn	Thr	Val	Pro	Val	
	450					455					460					
Tyr	Met	Pro	Phe	Ile	Thr	Ser	Tyr	Phe	Met	Pro	Arg	Val	Lys	Gly	Asp	
465					470					475					480	
Arg	Pro	Asp	Val	Val	Pro	Glu	Gly	Ser	Ala	Asn	Leu	Ala	Phe	Ile	Gly	
				485					490					495		
Asn	Phe	Ala	Glu	Ser	Pro	Ser	Arg	Asp	Thr	Val	Phe	Thr	Thr	Glu	Tyr	
		500						505					510			
Ser	Val	Arg	Thr	Ala	Met	Glu	Ala	Val	Tyr	Thr	Leu	Leu	Asp	Val	Asp	
	515						520					525				
Arg	Gly	Val	Pro	Glu	Val	Phe	Asn	Ser	Ile	Tyr	Asp	Leu	Arg	Glu	Leu	
	530					535					540					
Met	Arg	Ala	Met	Tyr	Tyr	Met	Asn	Asp	Lys	Lys	Pro	Leu	Lys	Asp	Met	
545					550					555					560	
Asp	Leu	Pro	Ile	Pro	Lys	Ile	Val	Glu	Lys	Pro	Leu	Leu	Lys	Lys	Leu	
				565					570					575		
Gln	Gly	Thr	Trp	Ile	Gly	Glu	Leu	Met	Glu	Gln	Gln	His	Leu	Leu		
			580					585					590			

<210> 19

<211> 656

<212> DNA

<213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(654)

<400> 19

atg gtc atg aca gaa act gct ggt ata aga aaa att cat att gtt ttt	48
Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe	
1 5 10 15	
gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca	96
Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser	
20 25 30	
caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac	144
Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp	
35 40 45	
ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta	192
Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu	
50 55 60	
agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag	240
Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys	
65 70 75 80	
gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct	288
Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala	
85 90 95	
aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat	336
Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn	
100 105 110	
aat ctt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag	384
Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys	
115 120 125	
ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt	432
Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu	
130 135 140	
ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa	480
Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln	
145 150 155 160	
ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac	528
Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn	
165 170 175	
ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc	576
Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe	
180 185 190	
ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga	624
Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly	
195 200 205	
aag aaa gat cag gat agc ggt aag gga ccg gt	656
Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro	
210 215	

<210> 20
 <211> 218
 <212> PRT
 <213> Lactobacillus reuteri

<400> 20
 Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125
 Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160
 Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175
 Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
 180 185 190
 Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly
 195 200 205
 Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro
 210 215

<210> 21
 <211> 726
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(726)

<220>
 <221> unsure
 <222> (1)..(726)
 <223> n = a, c, g, or t

<400> 21

atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca	48
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro	
1 5 10 15	
gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat	96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn	
20 25 30	
tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc	144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr	
35 40 45	
tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt	192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu	
50 55 60	
aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt	240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg	
65 70 75 80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg	288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg	
85 90 95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg	336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp	
100 105 110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat	384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn	
115 120 125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt	432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly	
130 135 140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg	480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr	
145 150 155 160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa	528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln	
165 170 175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa	576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln	
180 185 190	
gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg	624
Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro	
195 200 205	
gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac	672
Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr	
210 215 220	

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca 720
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

acc ggt
 Thr Gly 726

<210> 22
 <211> 242
 <212> PRT
 <213> Lactobacillus reuteri

<220>
 <221> UNSURE
 <222> (1)..(242)
 <223> Xaa = Tyr or stop

<400> 22
 Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
 1 5 10 15
 Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
 20 25 30
 Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
 35 40 45
 Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60
 Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
 65 70 75 80
 Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
 85 90 95
 Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110
 Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
 115 120 125
 His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
 130 135 140
 Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
 145 150 155 160
 Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
 165 170 175
 Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
 180 185 190
 Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220

Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

Thr Gly

<210> 23
 <211> 18
 <212> DNA
 <213> Lactobacillus reuteri

<400> 23
 aatctagtga tggttctc

18

<210> 24
 <211> 18
 <212> DNA
 <213> Lactobacillus reuteri

<400> 24
 caagttgagg aaggaaag

18

<210> 25
 <211> 3684
 <212> DNA
 <213> Lactobacillus reuteri

<400> 25
 caagttgagg aaggaaagaa agatcaggat agcggtaagg gaccgggttat ccttgataat 60
 gaaacaacag ataagatcgc tgaaacagac atgggtggatc tgttgaagca tgaccttcag 120
 catgatattg accataatct tgttcctgaa atgatacaca agtcaatgcg tgataattacc 180
 ataaatcggt ctcaagcaaa ggagaaaatt gctaagcagg ttaagcaaca tgatacgatt 240
 tatactttgc aaaaagaagc ggtctctcct cgggcagcta agccaaaact aaagactcga 300
 gaaaaaatta ccaagcaggc tcaggatgct ttgatcagtg gaatgtcacc acagcaacgg 360
 gatgctgaga aaaagtacac gacttttctg tacgatcggc caatggaacg aaacattgcg 420
 aataacaata gtggcctata cgttcctaata gatacgggaa ctaccccaat cccatttggt 480
 aaaattgcaa ctatttctga aattcgtgac gggttaaaga gcattgatgc tgttatgaag 540
 ggctatcagc agtttgctgt tgattatgat gctgactacg ggaagcgggt ctttgaagca 600
 attttgtata gttttactgc accgttttta tgggaaattc gttctaaagc tagcctgaac 660
 cctgaagatg ggaatgatgt tcctaatttc ctaatcctag gggcaacggc tggttccgga 720
 aagtctaccc ttcttcggat tattaatcag ctacagtgga acactgatcg ctcggttgatt 780
 gactttggaa cgatctaccc gtcgcaaaact cctcaaaaga aggcaaagac tgttgaggcg 840
 atggaacatt atatgaaact tggtagttca taccgggttt tgtagatga aattgaaccg 900
 tacttcttcc agcaagatca atagatcga ctggagttct gggttgctat gattaagggtt 960
 gttacgatta ttgcaatgat tattcttggt ttactgggta tcgttcttgg gttaggtaat 1020
 aactggcacc cagttgggat ttctaatttg tgggtctcatg gcggattctt taccgggtggc 1080
 tttatgggct ttatgttctc gctatctgtg attgctgggt cttatcaggg aattgagtta 1140
 ttgggaatca ctgctgggtga agctgaatca ccacgtcatg cgattgtgaa atcagtttaag 1200
 tccgttatct ggcggatctt aatcttctat attgggtgcaa ttttcgtcat tgtttctatt 1260
 taccatgga acgaattgaa gtccgttggc tcaccattcg ttgaaacctt cacgaagggt 1320
 ggaattactg gagcagccgg aatcattaac tttgttggtt tgacggcagc tctttctgga 1380
 gctaactctg gaatttacag tgctagtcgg atgttggtca agctttctgt tgatggggaa 1440
 gtaccaaagt tctttagtaa gctttccaag cgcgttggtc ctaatgttgc aatcctcacg 1500
 atttcttctt ggaatttctt tggctttgta attaatgaat taatgtcgat ttttagttct 1560
 gctgctcaaa atattttcgt cattgtatat agttccagtg ttcttcagg gatggtacca 1620
 tggtttatca ttctctgtc agaacttcac ttcagaaaag aacaccctga acagcttaaa 1680

gatcatccat	tcaagatgcc	gctttaccog	gcttataact	actttagttt	gattgccttg	1740
actgtgatct	tgatcttcat	gttctttaac	ccagatactc	gagtttcagt	atcagttggt	1800
gttatcttct	tgattatcat	gagtattatt	tatcgtgttc	gtgttcatga	aggaaaagaa	1860
aagtaaatat	atagctaaag	cagctttgta	aatcctgcgt	acaatacccc	ttagggttga	1920
cactttaaat	aataaaagt	tgaatcctag	ggggtgtttt	gcattgtaag	ttattcaact	1980
attgaaaagc	ttaaattact	tcatgattat	cagaaatcgg	attatggttt	aacggtgtac	2040
tccgattacc	atggtgtccg	accagcaaac	atgagtaagt	ggattaagca	attcctactc	2100
gctggattgg	cgggattaat	tagacctaa	cataatcaga	agtactcatt	agagactaag	2160
ttaactgctg	taaaagctta	tctttctggc	aagtatacta	atcaagcaat	tctccagcag	2220
tatcaaatta	gaaatatttc	tcaactacat	caatgggtta	tcagttacaa	taatgacaaa	2280
ctccgagtta	atcagacaac	gagaaagcga	gtcagaaaaa	tgggacgaaa	agtaaccttt	2340
gatgaaaaga	ggcagattgt	ccgatggaca	attgaacata	acaataacta	taaagcggct	2400
gcagagaagt	atgatattag	ttaccaacga	gtttattctt	gggtacggaa	gtaccgagta	2460
aatagcgact	gggaagtact	aaaagataac	cgtgggcgta	ataaaggaaa	agagcccact	2520
aatgaactag	aaaaactaag	gaaacgagtt	cgtgagctag	aagatcgtga	ccgtgaacgg	2580
gagctgcaaa	tcgctttcgc	aaaaaaatta	gtcgaaatac	gcaatcggga	ggtgaaacga	2640
ccggacgata	tcaagcgatt	caagaaatga	acaatgaagg	ttattccatt	agtgaattgg	2700
ccaaggtcgc	tgggaattact	agacaggctt	actacaaatg	gttgaaacat	gaaccgacta	2760
aatatgagat	tgaagaatcg	gagattctcc	aattgattaa	acagttagaa	aatgaacata	2820
agcaaagcgt	tggttatgac	aaaatgacta	ggttaatcaa	gttaagtcag	cagatctctt	2880
ataccgttaa	taagaaacga	gtcattcgtt	ttatgaaagg	ccatagtatc	aaggccgact	2940
atcgtcagcc	aaccgacaaa	cgtattcaag	cccagcaaac	ttatgaagct	gaaaatatct	3000
ttaaccgaca	atttgaccaa	actgcagcta	accaagtttg	ggttacggat	acgacggaac	3060
tgaattacgg	aatctggctt	aataaagttc	gtctacatat	agtattagat	ttatatggtc	3120
aatacccagt	aagctggtta	attacaccta	cagaaaccgc	tgaaggagta	gttcaagtgt	3180
tcgagcaagc	acggatgaaa	gaaggagcac	tagctccggt	aattcatact	gatcgtgggt	3240
cggcgtatac	ttccaaagca	tttaatcagt	atttagtagt	taatgggtgcc	caacacagtt	3300
attcagcacc	agggacaccg	gctgacaatg	ccgtaataga	acattggtgg	gcagatttta	3360
aggctatttg	gatcgcacat	ctacctaaag	cacaaacatt	attagaacta	gaagaacaag	3420
ttagagaagg	aattacctat	ttcactgaaa	aatttatctc	agcgaagaga	aatgacctta	3480
ccgcagcgga	ataccgcttt	ggcaaggcca	actaattttt	attatttaat	gtgtaaactt	3540
gacagggcac	agtaccctgt	ttgaggggac	tcacaaagct	gcttttttag	ttttgtttta	3600
ctgcaccggt	tgaataatta	atggtaatgt	ttctttggac	attcggaaac	aagacattgt	3660
attctagaga	accatcacta	gatt				3684

<210> 26

<211> 7113

<212> DNA

<213> Lactobacillus reuteri

<220>

<221> unsure

<222> (1)..(7113)

<223> n = a, c, g, or t

<400> 26

gtcgactgga	gttctgggtt	gctatgatta	aggttgttac	gattattgca	atgattattc	60
ttggtttact	ggttatcggt	cttggggttag	gtaataactg	gcaccagtt	gggatttcta	120
atttgtgggc	tcattggcga	ttctttaccg	gtggctttat	gggctttatg	ttctcgctat	180
ctgtgattgc	tggttcttat	cagggaattg	agttattggg	aatcactgct	ggtgaagctg	240
aatcaccacg	tcattgcgatt	gtgaaatcag	ttaaagtccg	tatctggcgg	atcttaattc	300
tctatattgg	tgcaattttc	gtcattgttt	ctatttacc	atggaacgaa	ttgaagtccg	360
ttggctcacc	attcgttgaa	accttcacga	aggttggaat	tactggagca	gccggaatca	420
ttaactttgt	tgttttgacg	gcagctcttt	ctggagctaa	ctctggaatt	tacagtgcta	480
gtcggatggt	gttcaagctt	tctgttgatg	gggaagtacc	aaagtctttt	agtaagcttt	540
ccaagcgcgt	tgttccta	gttgcaatcc	tcacgatttc	ttcctggatc	ttccttggct	600
ttgtaattaa	tgaattaatg	tcgattttta	gttctgctgc	tcaaaatatt	ttcgtcattg	660
tatatagttc	cagtgttctt	ccagggatgg	taccattggt	tatcattctc	ttgtcagaac	720
ttcacttcag	aaaagaacac	cctgaacagc	ttaaagatca	tccattcaag	atgccgcttt	780
acccggctta	taactacttt	agtttgattg	ccttgactgt	gatcttgatc	ttcatgttct	840

ttaaccagag	tactcgagtt	tcagtatcag	ttgggtggtat	cttcttgatt	atcatgagta	900
ttatttatcg	tggtcgtggt	catgaaggaa	aagaaaagta	aatatatagc	taaagcagct	960
ttgtaaatcc	tgcgtaacaat	acccttagg	gttgacactt	taaataataa	aagtgtgaat	1020
cctagggggt	gttttgcat	gtaagttatt	caactattga	aaagcttaaa	ttacttcatg	1080
attatcagaa	atcggtatt	ggtttaacgg	tgtactccga	ttaccatggt	gtccgaccag	1140
caaacatgag	taagtggatt	aagcaattcc	tactcgctgg	attggcgagg	tttaattagac	1200
ctaagcataa	tcagaagtac	tcattagaga	ctaagttaac	tgctgtaaaa	gcttatcttt	1260
ctggcaagta	tactaatcaa	gcaattctcc	agcagtatca	aattagaaat	atcttctcaac	1320
tacatcaatg	ggttatcagt	tacaataatg	acaaactccg	agttaatcag	acaacgagaa	1380
agcgagtcag	aaaaatggga	cgaaaagtaa	cctttgatga	aaagaggcag	attgtccgat	1440
ggacaattga	acataacaat	aactataaag	cggtgcaga	gaagtatgat	attagttacc	1500
aacgagttta	ttcttggtga	cggaagtacc	gagtaaatag	cgactgggaa	gtactaaaag	1560
ataaccgtgg	gcgtaataaa	ggaaaagagc	ccactaatga	actagaaaaa	ctaaggaaaa	1620
gagttcgtga	gctagaagat	cgtgaccgtg	aacgggagct	gcaaactcgct	ttcgcaaaaa	1680
aattagtcga	aatacgcaat	cgggaggtga	aacgaccgga	cgatatcaag	cgattcaaga	1740
aatgaacaat	gaaggttatt	ccattagtga	attggccaag	gtcgctggaa	ttactagaca	1800
ggcttactac	aaatggttga	aacatgaacc	gactaaatat	gagattgaag	aatcgagat	1860
tctccaattg	attaaacagt	tagaaaatga	acataagcaa	agcgttggtt	atgacaaaat	1920
gactaggtta	atcaagttaa	gtcagcagat	ctcttatacc	gttaataaga	aacgagtcac	1980
tcgtattatg	aaaggccata	gtatcaaggc	cgactatcgt	cagccaaccg	acaaacgtat	2040
tcaagcccag	caaacttatg	aagctgaaaa	tattcttaac	cgacaatttg	accaaactgc	2100
agctaaccac	gtttgggtta	cggatagcac	ggaactgaat	tacggaatct	ggcttaataa	2160
agttcgtcta	catatagtat	tagatttata	tggtcaatac	ccagtaagct	ggtaattac	2220
acctacagaa	accgctgaag	gagtagttca	agtgttcgag	caagcacgga	tgaaagaagg	2280
agcactagct	ccgttaattc	atactgatcg	tggtgcggcg	tatacttcca	aagcatttaa	2340
tcagtattta	gtagttaatg	gtgcccacaa	cagttattca	gcaccaggga	caccggctga	2400
caatgccgta	atagaacatt	ggtgggcaga	ttttaaggct	atgttgatcg	cacatctacc	2460
taaagcacia	acattattag	aactagaaga	acaagttaga	gaaggaatta	cctatttcac	2520
tgaaaaattt	atctcagcga	agagaaatga	ccttaccgca	gcggaatacc	gctttggcaa	2580
ggccaactaa	tttttattat	ttaatgtgta	aacttgacag	ggcacagtac	ctggtttgag	2640
gggactcaca	aagctgcttt	tttagttttg	ttttactgca	ccggttgaat	aattaatggt	2700
aatgtttctt	tggacattcg	gaacaaagac	attgtattct	agagaacat	cactagattt	2760
agcttcgata	tgagcacctg	ccggaacgat	attattaccg	tcataaatat	tggttaactcg	2820
gtagcgaact	tgcttattct	gatctaattg	ttttctcacc	agaccttcgt	agtaattttg	2880
ccctgttgag	ttcttacttc	gtgcttcatt	tgcccaggca	gtttgcgtgg	caatattaga	2940
tggtattgat	tcggatgcat	caaattccat	aataaccacca	actagtgcac	aggcaagaag	3000
gtgtccgcga	tcgtatgcat	gattgtatcc	gcctttaaga	ttatgcccct	gaaggaagcc	3060
agctggctgc	caatccgtag	caccattccc	tgtggcaaat	ttcggttnt	atattgaccg	3120
agttgtcctg	tttaaccagg	catcaccttg	ccacgcctt	ccttgacggt	caagatgatt	3180
tacagcatag	ggtgcacttg	caatcttagc	gttaagattt	gtttgggtat	tattgataat	3240
aaacgcaccg	gctttgttcc	aggtaattga	aatgccaaat	tggtggcgaa	cagccggagt	3300
taagactgaa	ttagcctggt	cctgagttgg	cggtaatgtt	tttttgatcg	ttgtgactgg	3360
ttttcttcca	ataagcaatt	ttactaatat	ggtntaacga	agcatttggt	agctgaggtt	3420
gctggataac	tccagtaact	actaataaac	cagcaagagc	aaataaaaag	tgatagaggc	3480
gtttcttaag	tttcataaat	tcactccatt	tctaataatt	ccaaagtcta	ttttactagt	3540
ttgaacatac	gtttggaata	attattttaga	attaatttat	aagttcattg	tgtttaataa	3600
aattgacact	ttcaaccgct	ttcactaaaa	ttaaggtagt	tatgatgcac	ttgtttactg	3660
agaagggagt	cgtcaaaatg	tattattcaa	acgggaatta	tgaagccttt	gctcgaccaa	3720
agaagcctgc	tggcgttgat	aagaaacatg	cctacattgt	cggtggtggt	ttagctggtt	3780
tatcggccgc	cgtgttttta	attcgtgatg	cccaaattgc	gggtgagaat	atccatattt	3840
tagaggaatt	accggttgcc	ggtggttctc	ttgatggtga	agatcgtcct	ggaattggtt	3900
ttgttactcg	tggagccggg	gaaatggaga	accatttcga	gtgtatgtgg	gacatgtatc	3960
gttcaattcc	atcacttgaa	atcccagggt	cttctacct	tgatgaatac	tactggttag	4020
ataaggaaga	tccaaacagt	tctaattgtc	gtttaacccta	taagcgggga	aatgaagttc	4080
catcgagcgg	taaatatggt	ttaagtaaaa	aggcaatcaa	agagctgact	aagctaatta	4140
tgaccctcga	agaaaaattg	ggaagggaga	ctattggtga	atacttctct	gatgatttct	4200
ttgaaagcaa	tttctggatt	tattggtcaa	caatgtttgc	gtttgaacgg	tggtcactctc	4260
tagctgaaat	gcgtcggtat	atgatgcggt	ttattcacca	tattgatggt	ttaccggatt	4320
tcactgcact	gaagttaaat	aagtataacc	aatatgaatc	aatgaccaag	ccgctattgg	4380
cctacctgaa	agatcatcat	gtcaagattg	agtacgatac	ccaggtaaaag	aatgttattg	4440
ttgatactca	tgggcggcaa	aagcacgcta	agcgaatctt	attaactcaa	gccggtaaaag	4500

ataaagttgt	tgagttaacg	gacaatgacc	ttgtctttgt	cacaaacggt	tcaattacag	4560
aaagttctac	ttacggcagt	caccatcaag	cagctcgacc	aacgcaagca	cttgggtggt	4620
gttggaaact	gtgggaaaac	cttgctcggc	agtcagctga	ttttgggtcat	cctgatgtct	4680
tttgcaagaa	tcttccaggg	agaagctggg	tcatttccgc	tactgcaacc	gttaagaacc	4740
cgcaagttga	accatacatt	gaacgcttaa	ccaagcgaga	tctccatgat	ggcaaagtta	4800
atactggtgg	aatcattacg	gtcactgact	ctaattggat	gctttcctgg	acaattcacc	4860
gtcaaccgca	cttcaagaaa	caaaagaaaa	atgaaacat	tgtttggatt	tacggtctgt	4920
actctaatac	aaagggaaaac	tatattaaga	aacggatcgt	tgattgtact	ggtgaagaga	4980
ttactaaaga	atggctatcc	atctgggggt	tccagaagcc	gttaattgac	gatttggcta	5040
aggagagttc	aattaatact	gttccagtat	atatgccatt	tatcactagc	tactttatgc	5100
cacgagttaa	gggcgaccgt	ccagacgttg	ttccagaagg	atccgctaac	ttggcattta	5160
ttggtaactt	tgctgaatct	ccaagtcgag	ataccgtatt	taccacggaa	tattcagtag	5220
ggaccgcaat	ggaagccgtc	tacactctat	tagatgttga	tcggggagtt	ccagaagtct	5280
ttactctat	ttatgatctt	cgagagttaa	tgcgggcaat	gtattacatg	aatgataaga	5340
agccgttaaa	agacatggac	ttgccaattc	caaagattgt	tgaaaagcca	ttattaaaga	5400
aactccaagg	aacgtggatt	ggtgaattaa	tggagcaaca	gcacttacta	taaagatgaa	5460
agaagctgga	aatttccggc	ttcttttttt	atatagctta	tcggggaacc	acttgcaaaa	5520
agggattaaa	tagtcgaaaa	taaaactaat	atattttattg	atagtaaagg	attatggtca	5580
tgacagaaac	tgctgggtata	agaaaaattc	atattgtttt	tgatggtcaa	gaaacaccac	5640
cattaaagat	ccatcaatta	tttgattcac	aaaaatacga	tcagttaatc	gcagtaactg	5700
ggaaaattac	tgctgacttc	attaataaat	accttagtaa	ttttatcagt	attaatgtag	5760
cgttaagctc	ccaatcaact	agtgaattaa	gtgctgatga	gatggtgaca	aagggtgcac	5820
ttaccaatgc	tctccttagt	tcagcaataa	aagaagctgc	taaactcttc	tcagcggttaa	5880
ccagtgacaa	ccaaacgaac	gtcttaataa	atctttttcg	cgtatcaatc	gcgcctactc	5940
aggttatcca	ttctaagttt	tacttgttaa	gtagttcaac	tactcatgat	tcccgtgtga	6000
ttcttgggag	tgtagattta	gacgaagctt	catttgatgc	tcaccgaaat	caatttgaag	6060
aagtattggt	atttgacaat	gatgtccgct	tataccaaaa	ccttactgac	cactttaaaa	6120
aggattttta	gccagtattg	aagcccttct	ttactatgaa	cctagttaaag	gcagctcaaa	6180
agcaagttga	ggaaggaaaag	aaagatcagg	atagcggtaa	gggaccggtt	atccttgata	6240
atgaaacaac	agataagatc	gctgaaacag	acatggtgga	tctgttgaag	catgaccttc	6300
agcatgatat	tgaccataat	cttgttcctg	aaatgatcac	aaagtcaatg	cgtgatatta	6360
ccataaatcg	ttctcaagca	aaggagaaaa	ttgctaagca	ggttaagcaa	catgatacga	6420
tttatacttt	gcaaaaagaa	gcggtctctc	ctcgggcagc	taagccaaaa	ctaaagactc	6480
gagaaaaaat	taccaagcag	gttcaggatg	ctttgatcag	tggaatgtca	ccacagcaac	6540
gggatgctga	gaaaaagtac	acgacttttc	tgtacgatcg	gccaatggaa	cgaaacattg	6600
cgaataacaa	tagtggccta	tacgttccta	atgatacggg	aactcaccca	atcccatttg	6660
gtaaaattgc	aactatttct	gaaattcgtg	acggtttaaa	gagcattgat	gctggttatg	6720
agggtatca	gcagtttgtc	gttgattatg	atgctgacta	cggggaagcg	ttctttgaag	6780
caattttgta	tagttttact	gcaccgtttt	tatgggaaat	tcgttctaaa	gctagcctga	6840
accctgaaga	tgggaatgat	gttcctaatt	tcctaatacct	aggggcaacg	gctggttccg	6900
gaaagtctac	ccttcttcgg	attattaatc	agctcacgtg	gaacactgat	cgctcgttga	6960
ttgacttttg	aacgatctac	ccgtcgcaaa	ctcctcaaaa	gaaggcaaag	actggtgagg	7020
cgatggaaca	ttatatgaaa	cttggtagtt	catacccggt	tttggttagat	gaaattgaac	7080
cgtacttctt	ccagcaagat	caatatagtc	gac			7113

<210> 27

<211> 941

<212> DNA

<213> *Lactobacillus reuteri*

<220>

<221> CDS

<222> (3)..(941)

<400> 27

gt	cga	ctg	gag	ttc	tgg	ttt	gct	atg	att	aag	ggt	ggt	acg	att	att	47
	Arg	Leu	Glu	Phe	Trp	Phe	Ala	Met	Ile	Lys	Val	Val	Thr	Ile	Ile	
1						5					10				15	

gca	atg	att	att	ctt	ggt	tta	ctg	ggt	atc	ggt	ctt	ggg	tta	ggt	aat	95
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Ala Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn	
20 25 30	
aac tgg cac cca gtt ggg att tct aat ttg tgg tct cat ggc gga ttc	143
Asn Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe	
35 40 45	
ttt acc ggt ggc ttt atg ggc ttt atg ttc tcg cta tct gtg att gct	191
Phe Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala	
50 55 60	
ggt tct tat cag gga att gag tta ttg gga atc act gct ggt gaa gct	239
Gly Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala	
65 70 75	
gaa tca cca cgt cat gcg att gtg aaa tca gtt aag tcc gtt atc tgg	287
Glu Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp	
80 85 90 95	
cgg atc tta atc ttc tat att ggt gca att ttc gtc att gtt tct att	335
Arg Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile	
100 105 110	
tac cca tgg aac gaa ttg aag tcc gtt ggc tca cca ttc gtt gaa acc	383
Tyr Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr	
115 120 125	
ttc acg aag gtt gga att act gga gca gcc gga atc att aac ttt gtt	431
Phe Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val	
130 135 140	
gtt ttg acg gca gct ctt tct gga gct aac tct gga att tac agt gct	479
Val Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala	
145 150 155	
agt cgg atg ttg ttc aag ctt tct gtt gat ggg gaa gta cca aag ttc	527
Ser Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe	
160 165 170 175	
ttt agt aag ctt tcc aag cgc gtt gtt cct aat gtt gca atc ctc acg	575
Phe Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr	
180 185 190	
att tct tcc tgg atc ttc ctt ggc ttt gta att aat gaa tta atg tcg	623
Ile Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser	
195 200 205	
att ttt agt tct gct gct caa aat att ttc gtc att gta tat agt tcc	671
Ile Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser	
210 215 220	
agt gtt ctt cca ggg atg gta cca tgg ttt atc att ctc ttg tca gaa	719
Ser Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu	
225 230 235	
ctt cac ttc aga aaa gaa cac cct gaa cag ctt aaa gat cat cca ttc	767
Leu His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe	
240 245 250 255	
aag atg ccg ctt tac ccg gct tat aac tac ttt agt ttg att gcc ttg	815
Lys Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu	

	260	265	270	
act gtg atc ttg atc ttc atg ttc ttt aac cca gat act cga gtt tca				863
Thr Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser				
	275	280	285	
gta tca gtt ggt gtt atc ttc ttg att atc atg agt att att tat cgt				911
Val Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg				
	290	295	300	
gtt cgt gtt cat gaa gga aaa gaa aag taa				941
Val Arg Val His Glu Gly Lys Glu Lys				
	305	310		

<210> 28
 <211> 312
 <212> PRT
 <213> *Lactobacillus reuteri*

<400> 28

Arg Leu Glu Phe Trp Phe Ala Met Ile Lys Val Val Thr Ile Ile Ala				
1 5 10 15				
Met Ile Ile Leu Gly Leu Leu Val Ile Val Leu Gly Leu Gly Asn Asn				
20 25 30				
Trp His Pro Val Gly Ile Ser Asn Leu Trp Ser His Gly Gly Phe Phe				
35 40 45				
Thr Gly Gly Phe Met Gly Phe Met Phe Ser Leu Ser Val Ile Ala Gly				
50 55 60				
Ser Tyr Gln Gly Ile Glu Leu Leu Gly Ile Thr Ala Gly Glu Ala Glu				
65 70 75 80				
Ser Pro Arg His Ala Ile Val Lys Ser Val Lys Ser Val Ile Trp Arg				
85 90 95				
Ile Leu Ile Phe Tyr Ile Gly Ala Ile Phe Val Ile Val Ser Ile Tyr				
100 105 110				
Pro Trp Asn Glu Leu Lys Ser Val Gly Ser Pro Phe Val Glu Thr Phe				
115 120 125				
Thr Lys Val Gly Ile Thr Gly Ala Ala Gly Ile Ile Asn Phe Val Val				
130 135 140				
Leu Thr Ala Ala Leu Ser Gly Ala Asn Ser Gly Ile Tyr Ser Ala Ser				
145 150 155 160				
Arg Met Leu Phe Lys Leu Ser Val Asp Gly Glu Val Pro Lys Phe Phe				
165 170 175				
Ser Lys Leu Ser Lys Arg Val Val Pro Asn Val Ala Ile Leu Thr Ile				
180 185 190				
Ser Ser Trp Ile Phe Leu Gly Phe Val Ile Asn Glu Leu Met Ser Ile				
195 200 205				
Phe Ser Ser Ala Ala Gln Asn Ile Phe Val Ile Val Tyr Ser Ser Ser				
210 215 220				
Val Leu Pro Gly Met Val Pro Trp Phe Ile Ile Leu Leu Ser Glu Leu				
225 230 235 240				
His Phe Arg Lys Glu His Pro Glu Gln Leu Lys Asp His Pro Phe Lys				
245 250 255				
Met Pro Leu Tyr Pro Ala Tyr Asn Tyr Phe Ser Leu Ile Ala Leu Thr				
260 265 270				
Val Ile Leu Ile Phe Met Phe Phe Asn Pro Asp Thr Arg Val Ser Val				
275 280 285				
Ser Val Gly Val Ile Phe Leu Ile Ile Met Ser Ile Ile Tyr Arg Val				
290 295 300				
Arg Val His Glu Gly Lys Glu Lys				
305 310				

<210> 29
 <211> 600
 <212> DNA
 <213> *Lactobacillus reuteri*

<220>
 <221> CDS
 <222> (1)..(597)

<400> 29
 atg agt aag tgg att aag caa ttc cta ctc gct gga ttg gcg gga tta 48
 Met Ser Lys Trp Ile Lys Gln Phe Leu Leu Ala Gly Leu Ala Gly Leu
 1 5 10 15
 att aga cct aag cat aat cag aag tac tca tta gag act aag tta act 96
 Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr
 20 25 30
 gct gta aaa gct tat ctt tct ggc aag tat act aat caa gca att ctc 144
 Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
 35 40 45
 cag cag tat caa att aga aat att tct caa cta cat caa tgg gtt atc 192
 Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
 50 55 60
 agt tac aat aat gac aaa ctc cga gtt aat cag aca acg aga aag cga 240
 Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
 65 70 75 80
 gtc aga aaa atg gga cga aaa gta acc ttt gat gaa aag agg cag att 288
 Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
 85 90 95
 gtc cga tgg aca att gaa cat aac aat aac tat aaa gcg gct gca gag 336
 Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
 100 105 110
 aag tat gat att agt tac caa cga gtt tat tct tgg gta cgg aag tac 384
 Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
 115 120 125
 cga gta aat agc gac tgg gaa gta cta aaa gat aac cgt ggg cgt aat 432
 Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
 130 135 140
 aaa gga aaa gag ccc act aat gaa cta gaa aaa cta agg aaa cga gtt 480
 Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
 145 150 155 160
 cgt gag cta gaa gat cgt gac cgt gaa cgg gag ctg caa atc gct ttc 528
 Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
 165 170 175
 gca aaa aaa tta gtc gaa ata cgc aat cgg gag gtg aaa cga ccg gac 576
 Ala Lys Lys Leu Val Glu Ile Arg Asn Arg Glu Val Lys Arg Pro Asp
 180 185 190

gat atc aag cga ttc aag aaa tga
 Asp Ile Lys Arg Phe Lys Lys
 195

600

<210> 30
 <211> 199
 <212> PRT
 <213> Lactobacillus reuteri

<400> 30
 Met Ser Lys Trp Ile Lys Gln Phe Leu Leu Ala Gly Leu Ala Gly Leu
 1 5 10 15
 Ile Arg Pro Lys His Asn Gln Lys Tyr Ser Leu Glu Thr Lys Leu Thr
 20 25 30
 Ala Val Lys Ala Tyr Leu Ser Gly Lys Tyr Thr Asn Gln Ala Ile Leu
 35 40 45
 Gln Gln Tyr Gln Ile Arg Asn Ile Ser Gln Leu His Gln Trp Val Ile
 50 55 60
 Ser Tyr Asn Asn Asp Lys Leu Arg Val Asn Gln Thr Thr Arg Lys Arg
 65 70 75 80
 Val Arg Lys Met Gly Arg Lys Val Thr Phe Asp Glu Lys Arg Gln Ile
 85 90 95
 Val Arg Trp Thr Ile Glu His Asn Asn Asn Tyr Lys Ala Ala Ala Glu
 100 105 110
 Lys Tyr Asp Ile Ser Tyr Gln Arg Val Tyr Ser Trp Val Arg Lys Tyr
 115 120 125
 Arg Val Asn Ser Asp Trp Glu Val Leu Lys Asp Asn Arg Gly Arg Asn
 130 135 140
 Lys Gly Lys Glu Pro Thr Asn Glu Leu Glu Lys Leu Arg Lys Arg Val
 145 150 155 160
 Arg Glu Leu Glu Asp Arg Asp Arg Glu Arg Glu Leu Gln Ile Ala Phe
 165 170 175
 Ala Lys Lys Leu Val Glu Ile Arg Asn Arg Glu Val Lys Arg Pro Asp
 180 185 190
 Asp Ile Lys Arg Phe Lys Lys
 195

<210> 31
 <211> 849
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(849)

<400> 31

atg aac aat gaa ggt tat tcc att agt gaa ttg gcc aag gtc gct gga	48
Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly	
1 5 10 15	
att act aga cag gct tac tac aaa tgg ttg aaa cat gaa ccg act aaa	96
Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys	
20 25 30	
tat gag att gaa gaa tcg gag att ctc caa ttg att aaa cag tta gaa	144
Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu	
35 40 45	
aat gaa cat aag caa agc gtt ggt tat gac aaa atg act agg tta atc	192
Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile	
50 55 60	
aag tta agt cag cag atc tct tat acc gtt aat aag aaa cga gtc att	240
Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile	
65 70 75 80	
cgt att atg aaa ggc cat agt atc aag gcc gac tat cgt cag cca acc	288
Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr	
85 90 95	
gac aaa cgt att caa gcc cag caa act tat gaa gct gaa aat att ctt	336
Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu	
100 105 110	
aac cga caa ttt gac caa act gca gct aac caa gtt tgg gtt acg gat	384
Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp	
115 120 125	
acg acg gaa ctg aat tac gga atc tgg ctt aat aaa gtt cgt cta cat	432
Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His	
130 135 140	
ata gta tta gat tta tat ggt caa tac cca gta agc tgg tta att aca	480
Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr	
145 150 155 160	
cct aca gaa acc gct gaa gga gta gtt caa gtg ttc gag caa gca cgg	528
Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg	
165 170 175	
atg aaa gaa gga gca cta gct ccg tta att cat act gat cgt ggt gcg	576
Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala	
180 185 190	
gcg tat act tcc aaa gca ttt aat cag tat tta gta gtt aat ggt gcc	624
Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala	
195 200 205	
caa cac agt tat tca gca cca ggg aca ccg gct gac aat gcc gta ata	672
Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile	
210 215 220	
gaa cat tgg tgg gca gat ttt aag gct att tgg atc gca cat cta cct	720
Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro	
225 230 235 240	

aaa gca caa aca tta tta gaa cta gaa gaa caa gtt aga gaa gga att 768
 Lys Ala Gln Thr Leu Leu Glu Leu Glu Glu Gln Val Arg Glu Gly Ile
 245 250 255

acc tat ttc act gaa aaa ttt atc tca gcg aag aga aat gac ctt acc 816
 Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
 260 265 270

gca gcg gaa tac cgc ttt ggc aag gcc aac taa 849
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

<210> 32
 <211> 282
 <212> PRT
 <213> Lactobacillus reuteri

<400> 32
 Met Asn Asn Glu Gly Tyr Ser Ile Ser Glu Leu Ala Lys Val Ala Gly
 1 5 10 15
 Ile Thr Arg Gln Ala Tyr Tyr Lys Trp Leu Lys His Glu Pro Thr Lys
 20 25 30
 Tyr Glu Ile Glu Glu Ser Glu Ile Leu Gln Leu Ile Lys Gln Leu Glu
 35 40 45
 Asn Glu His Lys Gln Ser Val Gly Tyr Asp Lys Met Thr Arg Leu Ile
 50 55 60
 Lys Leu Ser Gln Gln Ile Ser Tyr Thr Val Asn Lys Lys Arg Val Ile
 65 70 75 80
 Arg Ile Met Lys Gly His Ser Ile Lys Ala Asp Tyr Arg Gln Pro Thr
 85 90 95
 Asp Lys Arg Ile Gln Ala Gln Gln Thr Tyr Glu Ala Glu Asn Ile Leu
 100 105 110
 Asn Arg Gln Phe Asp Gln Thr Ala Ala Asn Gln Val Trp Val Thr Asp
 115 120 125
 Thr Thr Glu Leu Asn Tyr Gly Ile Trp Leu Asn Lys Val Arg Leu His
 130 135 140
 Ile Val Leu Asp Leu Tyr Gly Gln Tyr Pro Val Ser Trp Leu Ile Thr
 145 150 155 160
 Pro Thr Glu Thr Ala Glu Gly Val Val Gln Val Phe Glu Gln Ala Arg
 165 170 175
 Met Lys Glu Gly Ala Leu Ala Pro Leu Ile His Thr Asp Arg Gly Ala
 180 185 190
 Ala Tyr Thr Ser Lys Ala Phe Asn Gln Tyr Leu Val Val Asn Gly Ala
 195 200 205
 Gln His Ser Tyr Ser Ala Pro Gly Thr Pro Ala Asp Asn Ala Val Ile
 210 215 220
 Glu His Trp Trp Ala Asp Phe Lys Ala Ile Trp Ile Ala His Leu Pro
 225 230 235 240
 Lys Ala Gln Thr Leu Leu Glu Leu Glu Glu Gln Val Arg Glu Gly Ile
 245 250 255
 Thr Tyr Phe Thr Glu Lys Phe Ile Ser Ala Lys Arg Asn Asp Leu Thr
 260 265 270
 Ala Ala Glu Tyr Arg Phe Gly Lys Ala Asn
 275 280

<210> 33
 <211> 744
 <212> DNA

<213> Lactobacillus reuteri

<220>

<221> CDS

<222> (1)..(744)

<220>

<221> unsure

<222> (1)..(744)

<223> n = a, c, g, or t

<400> 33

atg ctt cgt tan acc ata tta gta aaa ttg ctt att gga aga aaa cca	48
Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro	
1 5 10 15	
gtc aca acg atc aaa aaa aca tta ccg cca act cag gaa cag gct aat	96
Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn	
20 25 30	
tca gtc tta act ccg gct gtt cgc caa caa ctt ggc att tca att acc	144
Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr	
35 40 45	
tgg aac aaa gcc ggt gcg ttt att atc aat aat aac caa aca aat ctt	192
Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu	
50 55 60	
aac gct aag att gca agt gca ccc tat gct gta aat cat ctt gac cgt	240
Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg	
65 70 75 80	
caa gga agg gcg tgg caa ggt gat gcc tgg tta aac agg aca act cgg	288
Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg	
85 90 95	
tca ata tan aag ccg aaa ttt gcc aca ggg aat ggt gct acg gat tgg	336
Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp	
100 105 110	
cga cca gct ggc ttc ctt cag gcg cat aat ctt aaa ggc ggg tac aat	384
Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn	
115 120 125	
cat gca tac gat cgc gga cac ctt ctt gcc tat gca cta gtt ggt ggt	432
His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly	
130 135 140	
att cat gga ttt gat gca tcc gaa tca aat cca tct aat att gcc acg	480
Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr	
145 150 155 160	
caa act gcc tgg gca aat gaa gca cga agt aag aac tca aca ggg caa	528
Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln	
165 170 175	
aat tac tac gaa ggt ctg gtg aga aaa gca tta gat cag aat aag caa	576
Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln	
180 185 190	
gtt cgc tac cga gtt acc aat att tat gac ggt aat aat atc gtt ccg	624

Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205

gca ggt gct cat atc gaa gct aaa tct agt gat ggt tct cta gaa tac 672
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220

aat gtc ttt gtt ccg aat gtc caa aga aac att acc att aat tat tca 720
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240

acc ggt gca gta aaa caa aac taa 744
 Thr Gly Ala Val Lys Gln Asn
 245

<210> 34
 <211> 247
 <212> PRT
 <213> Lactobacillus reuteri

<220>
 <221> UNSURE
 <222> (1)..(247)
 <223> Xaa = Tyr or stop

<400> 34
 Met Leu Arg Xaa Thr Ile Leu Val Lys Leu Leu Ile Gly Arg Lys Pro
 1 5 10 15
 Val Thr Thr Ile Lys Lys Thr Leu Pro Pro Thr Gln Glu Gln Ala Asn
 20 25 30
 Ser Val Leu Thr Pro Ala Val Arg Gln Gln Leu Gly Ile Ser Ile Thr
 35 40 45
 Trp Asn Lys Ala Gly Ala Phe Ile Ile Asn Asn Asn Gln Thr Asn Leu
 50 55 60
 Asn Ala Lys Ile Ala Ser Ala Pro Tyr Ala Val Asn His Leu Asp Arg
 65 70 75 80
 Gln Gly Arg Ala Trp Gln Gly Asp Ala Trp Leu Asn Arg Thr Thr Arg
 85 90 95
 Ser Ile Xaa Lys Pro Lys Phe Ala Thr Gly Asn Gly Ala Thr Asp Trp
 100 105 110
 Arg Pro Ala Gly Phe Leu Gln Ala His Asn Leu Lys Gly Gly Tyr Asn
 115 120 125
 His Ala Tyr Asp Arg Gly His Leu Leu Ala Tyr Ala Leu Val Gly Gly
 130 135 140
 Ile His Gly Phe Asp Ala Ser Glu Ser Asn Pro Ser Asn Ile Ala Thr
 145 150 155 160
 Gln Thr Ala Trp Ala Asn Glu Ala Arg Ser Lys Asn Ser Thr Gly Gln
 165 170 175
 Asn Tyr Tyr Glu Gly Leu Val Arg Lys Ala Leu Asp Gln Asn Lys Gln
 180 185 190
 Val Arg Tyr Arg Val Thr Asn Ile Tyr Asp Gly Asn Asn Ile Val Pro
 195 200 205
 Ala Gly Ala His Ile Glu Ala Lys Ser Ser Asp Gly Ser Leu Glu Tyr
 210 215 220
 Asn Val Phe Val Pro Asn Val Gln Arg Asn Ile Thr Ile Asn Tyr Ser
 225 230 235 240
 Thr Gly Ala Val Lys Gln Asn
 245

<210> 35
 <211> 1540
 <212> DNA
 <213> Lactobacillus reuteri

<220>
 <221> CDS
 <222> (1)..(1539)

<400> 35
 atg gtc atg aca gaa act gct ggt ata aga aaa att cat att gtt ttt 48
 Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15
 gat ggt caa gaa aca cca cca tta aag atc cat caa tta ttt gat tca 96
 Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30
 caa aaa tac gat cag tta atc gca gta act ggg aaa att act gct gac 144
 Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45
 ttc att aat aaa tac ctt agt aat ttt atc agt att aat gta gcg tta 192
 Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60
 agc tcc caa tca act agt gaa tta agt gct gat gag atg gtg aca aag 240
 Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80
 gtt gca ctt acc aat gct ctc ctt agt tca gca aat aaa gaa gct gct 288
 Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95
 aaa ctc ttc tca gcg tta acc agt gac aac caa acg aac gtc tta aat 336
 Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110
 aat gtt ttt cgc gta tca atc gcg cct act cag gtt atc cat tct aag 384
 Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125
 ttt tac ttg tta agt agt tca act act cat gat tcc cgt gtg att ctt 432
 Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140
 ggg agt gta gat tta gac gaa gct tca ttt gat gct cac cga aat caa 480
 Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160
 ttt gaa gaa gta ttg gta ttt gac aat gat gtc cgc tta tac caa aac 528
 Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175
 ctt act gac cac ttt aaa aag gat ttt aag cca gta ttg aag ccc ttc 576
 Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe
 180 185 190
 ttt act atg aac cta gta aag gca gct caa aag caa gtt gag gaa gga 624
 Phe Thr Met Asn Leu Val Lys Ala Ala Gln Lys Gln Val Glu Glu Gly

195	200	205	
aag aaa gat cag gat agc ggt aag gga ccg gtt atc ctt gat aat gaa Lys Lys Asp Gln Asp Ser Gly Lys Gly Pro Val Ile Leu Asp Asn Glu 210 215 220			672
aca aca gat aag atc gct gaa aca gac atg gtg gat ctg ttg aag cat Thr Thr Asp Lys Ile Ala Glu Thr Asp Met Val Asp Leu Leu Lys His 225 230 235 240			720
gac ctt cag cat gat att gac cat aat ctt gtt cct gaa atg atc aca Asp Leu Gln His Asp Ile Asp His Asn Leu Val Pro Glu Met Ile Thr 245 250 255			768
aag tca atg cgt gat att acc ata aat cgt tct caa gca aag gag aaa Lys Ser Met Arg Asp Ile Thr Ile Asn Arg Ser Gln Ala Lys Glu Lys 260 265 270			816
att gct aag cag gtt aag caa cat gat acg att tat act ttg caa aaa Ile Ala Lys Gln Val Lys Gln His Asp Thr Ile Tyr Thr Leu Gln Lys 275 280 285			864
gaa gcg gtc tct cct cgg gca gct aag cca aaa cta aag act cga gaa Glu Ala Val Ser Pro Arg Ala Ala Lys Pro Lys Leu Lys Thr Arg Glu 290 295 300			912
aaa att acc aag cag gtt cag gat gct ttg atc agt gga atg tca cca Lys Ile Thr Lys Gln Val Gln Asp Ala Leu Ile Ser Gly Met Ser Pro 305 310 315 320			960
cag caa cgg gat gct gag aaa aag tac acg act ttt ctg tac gat cgg Gln Gln Arg Asp Ala Glu Lys Lys Tyr Thr Thr Phe Leu Tyr Asp Arg 325 330 335			1008
cca atg gaa cga aac att gcg aat aac aat agt ggc cta tac gtt cct Pro Met Glu Arg Asn Ile Ala Asn Asn Asn Ser Gly Leu Tyr Val Pro 340 345 350			1056
aat gat acg gga act cac cca atc cca ttt ggt aaa att gca act att Asn Asp Thr Gly Thr His Pro Ile Pro Phe Gly Lys Ile Ala Thr Ile 355 360 365			1104
tct gaa att cgt gac ggt tta aag agc att gat gct gtt atg aag ggc Ser Glu Ile Arg Asp Gly Leu Lys Ser Ile Asp Ala Val Met Lys Gly 370 375 380			1152
tat cag cag ttt gtc gtt gat tat gat gct gac tac ggg aag cgg ttc Tyr Gln Gln Phe Val Val Asp Tyr Asp Ala Asp Tyr Gly Lys Arg Phe 385 390 395 400			1200
ttt gaa gca att ttg tat agt ttt act gca ccg ttt tta tgg gaa att Phe Glu Ala Ile Leu Tyr Ser Phe Thr Ala Pro Phe Leu Trp Glu Ile 405 410 415			1248
cgt tct aaa gct agc ctg aac cct gaa gat ggg aat gat gtt cct aat Arg Ser Lys Ala Ser Leu Asn Pro Glu Asp Gly Asn Asp Val Pro Asn 420 425 430			1296
ttc cta atc cta ggg gca acg gct ggt tcc gga aag tct acc ctt ctt Phe Leu Ile Leu Gly Ala Thr Ala Gly Ser Gly Lys Ser Thr Leu Leu 435 440 445			1344

cgg att att aat cag ctc acg tgg aac act gat cgc tcg ttg att gac 1392
 Arg Ile Ile Asn Gln Leu Thr Trp Asn Thr Asp Arg Ser Leu Ile Asp
 450 455 460

ttt gga acg atc tac ccg tcg caa act cct caa aag aag gca aag act 1440
 Phe Gly Thr Ile Tyr Pro Ser Gln Thr Pro Gln Lys Lys Ala Lys Thr
 465 470 475 480

gtt gag gcg atg gaa cat tat atg aaa ctt ggt agt tca tac ccg gtt 1488
 Val Glu Ala Met Glu His Tyr Met Lys Leu Gly Ser Ser Tyr Pro Val
 485 490 495

ttg tta gat gaa att gaa ccg tac ttc ttc cag caa gat caa tat agt 1536
 Leu Leu Asp Glu Ile Glu Pro Tyr Phe Phe Gln Gln Asp Gln Tyr Ser
 500 505 510

cga c 1540
 Arg

<210> 36

<211> 513

<212> PRT

<213> Lactobacillus reuteri

<400> 36

Met Val Met Thr Glu Thr Ala Gly Ile Arg Lys Ile His Ile Val Phe
 1 5 10 15

Asp Gly Gln Glu Thr Pro Pro Leu Lys Ile His Gln Leu Phe Asp Ser
 20 25 30

Gln Lys Tyr Asp Gln Leu Ile Ala Val Thr Gly Lys Ile Thr Ala Asp
 35 40 45

Phe Ile Asn Lys Tyr Leu Ser Asn Phe Ile Ser Ile Asn Val Ala Leu
 50 55 60

Ser Ser Gln Ser Thr Ser Glu Leu Ser Ala Asp Glu Met Val Thr Lys
 65 70 75 80

Val Ala Leu Thr Asn Ala Leu Leu Ser Ser Ala Asn Lys Glu Ala Ala
 85 90 95

Lys Leu Phe Ser Ala Leu Thr Ser Asp Asn Gln Thr Asn Val Leu Asn
 100 105 110

Asn Leu Phe Arg Val Ser Ile Ala Pro Thr Gln Val Ile His Ser Lys
 115 120 125

Phe Tyr Leu Leu Ser Ser Ser Thr Thr His Asp Ser Arg Val Ile Leu
 130 135 140

Gly Ser Val Asp Leu Asp Glu Ala Ser Phe Asp Ala His Arg Asn Gln
 145 150 155 160

Phe Glu Glu Val Leu Val Phe Asp Asn Asp Val Arg Leu Tyr Gln Asn
 165 170 175

Leu Thr Asp His Phe Lys Lys Asp Phe Lys Pro Val Leu Lys Pro Phe

180										185					190				
Phe	Thr	Met	Asn	Leu	Val	Lys	Ala	Ala	Gln	Lys	Gln	Val	Glu	Glu	Gly				
		195					200					205							
Lys	Lys	Asp	Gln	Asp	Ser	Gly	Lys	Gly	Pro	Val	Ile	Leu	Asp	Asn	Glu				
	210					215					220								
Thr	Thr	Asp	Lys	Ile	Ala	Glu	Thr	Asp	Met	Val	Asp	Leu	Leu	Lys	His				
225					230					235					240				
Asp	Leu	Gln	His	Asp	Ile	Asp	His	Asn	Leu	Val	Pro	Glu	Met	Ile	Thr				
			245					250						255					
Lys	Ser	Met	Arg	Asp	Ile	Thr	Ile	Asn	Arg	Ser	Gln	Ala	Lys	Glu	Lys				
			260					265					270						
Ile	Ala	Lys	Gln	Val	Lys	Gln	His	Asp	Thr	Ile	Tyr	Thr	Leu	Gln	Lys				
		275					280					285							
Glu	Ala	Val	Ser	Pro	Arg	Ala	Ala	Lys	Pro	Lys	Leu	Lys	Thr	Arg	Glu				
	290					295					300								
Lys	Ile	Thr	Lys	Gln	Val	Gln	Asp	Ala	Leu	Ile	Ser	Gly	Met	Ser	Pro				
305				310						315					320				
Gln	Gln	Arg	Asp	Ala	Glu	Lys	Lys	Tyr	Thr	Thr	Phe	Leu	Tyr	Asp	Arg				
			325					330						335					
Pro	Met	Glu	Arg	Asn	Ile	Ala	Asn	Asn	Asn	Ser	Gly	Leu	Tyr	Val	Pro				
			340				345						350						
Asn	Asp	Thr	Gly	Thr	His	Pro	Ile	Pro	Phe	Gly	Lys	Ile	Ala	Thr	Ile				
		355				360						365							
Ser	Glu	Ile	Arg	Asp	Gly	Leu	Lys	Ser	Ile	Asp	Ala	Val	Met	Lys	Gly				
	370					375					380								
Tyr	Gln	Gln	Phe	Val	Val	Asp	Tyr	Asp	Ala	Asp	Tyr	Gly	Lys	Arg	Phe				
385				390					395						400				
Phe	Glu	Ala	Ile	Leu	Tyr	Ser	Phe	Thr	Ala	Pro	Phe	Leu	Trp	Glu	Ile				
			405					410						415					
Arg	Ser	Lys	Ala	Ser	Leu	Asn	Pro	Glu	Asp	Gly	Asn	Asp	Val	Pro	Asn				
			420					425					430						
Phe	Leu	Ile	Leu	Gly	Ala	Thr	Ala	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu				
	435						440					445							
Arg	Ile	Ile	Asn	Gln	Leu	Thr	Trp	Asn	Thr	Asp	Arg	Ser	Leu	Ile	Asp				
	450					455					460								
Phe	Gly	Thr	Ile	Tyr	Pro	Ser	Gln	Thr	Pro	Gln	Lys	Lys	Ala	Lys	Thr				
465					470				475					480					
Val	Glu	Ala	Met	Glu	His	Tyr	Met	Lys	Leu	Gly	Ser	Ser	Tyr	Pro	Val				
			485					490						495					
Leu	Leu	Asp	Glu	Ile	Glu	Pro	Tyr	Phe	Phe	Gln	Gln	Asp	Gln	Tyr	Ser				
		500						505					510						

Arg

BEST AVAILABLE COPY

<210> 37
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<220>
<221> terminator
<222> (1)..(26)

<400> 37
aaagaagctg aaatttcggc ttcttt

26

<210> 38
<211> 28
<212> DNA
<213> Lactobacillus reuteri

<400> 38
gcagtcgacg gagttaagac tgaattag

28

<210> 39
<211> 26
<212> DNA
<213> Lactobacillus reuteri

<400> 39
ctagtcgacg cagtttctgt catgac

26

<210> 40
<211> 32
<212> DNA
<213> Lactobacillus reuteri

<400> 40
catatgtatt attcaaacgg gaattatgaa gc

32

<210> 41
<211> 30
<212> DNA
<213> Lactobacillus reuteri

<400> 41
tgatcatcta taccagcagt ttctgtcatg

30

<210> 42
<211> 35
<212> PRT
<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (30)

<223> Xaa = any amino acid

<400> 42

Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro Ala
1 5 10 15

Gly Leu Ala Ala Gly Met Tyr Leu Trp Gln Ala Gly Phe Xaa Asp Tyr
20 25 30

Thr Ile Leu
35

<210> 43

<211> 21

<212> PRT

<213> Clostridium sporogenes

<220>

<221> UNSURE

<222> (18)

<223> Xaa = any amino acid

<400> 43

Met Phe Asn Leu Lys Asn Arg Asn Phe Leu Thr Leu Met Asp Phe Thr
1 5 10 15

Pro Xaa Glu Ile Gln
20

<210> 44

<211> 14

<212> PRT

<213> Propionibacterium acnes

<400> 44

Lys Tyr Leu Asp Phe Val Thr Met Met Ser Phe Ala Lys Gly
1 5 10

<210> 45

<211> 9

<212> PRT

<213> Propionibacterium acnes

<400> 45

Lys Asp Leu Val Thr Arg Phe Phe Val
1 5

<210> 46

<211> 15

<212> PRT

<213> Propionibacterium acnes

<220>

<221> UNSURE

<222> (2)

<223> Xaa = Ile or Ser

<220>

<221> UNSURE

<222> (4)

<223> Xaa = His or Phe

<220>

<221> UNSURE

<222> (6)

<223> Xaa = Glu or Gln

<220>

<221> UNSURE

<222> (10)

<223> Xaa = Asp or Thr

<220>

<221> UNSURE

<222> (12)

<223> Xaa = Gly or Ser

<400> 46

Lys	Xaa	Ile	Xaa	Gln	Xaa	Tyr	Met	Val	Xaa	Ala	Xaa	Leu	Val	Lys
1				5					10					15

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 47

atcgcgatna tnggngcngg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> unsure

<222> (1)..(20)

<223> n = a, c, g, or t

<400> 48

ccngcytgcc anarrtacat

20

<210> 49
<211> 62
<212> DNA
<213> Propionibacterium acnes

<400> 49
atcgagatva trggggctgg cccggccggg ctggctgccg gaatgtacct ctggcargcs 60
gg 62

<210> 50
<211> 21
<212> PRT
<213> Propionibacterium acnes

<220>
<221> UNSURE
<222> (2)
<223> xaa = ala or glu

<220>
<221> UNSURE
<222> (3)..(4)
<223> xaa = ile or met

<400> 50
Ile Xaa Xaa Xaa Gly Ala Gly Pro Ala Gly Leu Ala Ala Gly Met Tyr
1 5 10 15
Leu Trp Gln Ala Gly
20

<210> 51
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<220>
<221> unsure
<222> (1)..(17)
<223> n = a, c, g, or t

<400> 51
gggccagccc cyatnat

17

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 52
gctggctgcc ggaatgta

18

<210> 53
 <211> 569
 <212> DNA
 <213> Propionibacterium acnes

<400> 53
 ggatcccaac tggccgctg ccccggggga ggagtaccac gccgacatcg aaggcaacaa 60
 tgcccgtaac ggggtggaccg aggacacccc ggccgtcaat gatgccagg ccgagcggcg 120
 ggccaaggag ctggcagcac atctcgatga gatggcacgt ggtcggcgaa ctgcccgtg 180
 agatgtttcg cgacctatac cattaccgac ccatttcac gccgaactta ttcaccacta 240
 catcgacaag gaagaacgat gtccatctcg aaggattcac gtatcgccat catcggggct 300
 ggcccggccg ggctggctgc cggaatgtac ctggaacagg ccggatttca cgactacacg 360
 atcctggaac gcaccgacca cgtcggaggc aagtgccact caccgaacta ccacggccgt 420
 cgttatgaga tgggggcat catgggcgtc ccagttacg acaccatcca ggagatcatg 480
 gatcgactg gcgacaaggc cgacgggccc aaactgcgtc gcgagttcct gcacgaggac 540
 ggcgagatct acgtcccga aaaggatcc 569

<210> 54
 <211> 104
 <212> PRT
 <213> Propionibacterium acnes

<400> 54
 Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
 1 5 10 15
 Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
 20 25 30
 Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
 35 40 45
 Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
 50 55 60
 Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
 65 70 75 80
 Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
 85 90 95
 Ile Tyr Val Pro Glu Lys Asp Pro
 100

<210> 55
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 55
 cgatgtcggc gtggtac

<210> 56
 <211> 18

<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 56

tcacgtatcg ccatcatc

18

<210> 57

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 57

aatccggcct gttcgag

17

<210> 58

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 58

aggacggcga gatctac

17

<210> 59

<211> 5275

<212> DNA

<213> Propionibacterium acnes

<400> 59

gccggggcggg cacgattgac gaatttccgc aactgggatg gcggaacaaa ggtgtcgtga 60
tttccttgga tcaccattgt tgggtggtgcc tgaggagtga tccaggtgga actgttgaca 120
gcgcgataac ggtcggggaa ttgcttgggg gtgccaccga tatacatttt ggcggcattg 180
cccgcgtca gtgtggtgac cgactcgacg gtaccgacat ccaccgttg atagaggcg 240
aggactgact tcggggcccg tattgagccg caggaactct tcaactttcc actggcggcg 300
ccgtaggcga gattaatggc cattccacca ccagcgggat caccatgat cgatacctgt 360
gaaggggtcgc caccgagttc ttccacgtgg gacaggctcc agggccaggc acatgcgacc 420
tgttttgggg cggtattcca ggtgggggtgg ccctgggtgg ccagggtgta cgagggcgga 480
atgactaacc agccatgatc ggaaaacat ctcaacgtgg cgggcatggt gggtcggtg 540
ctccatcctt caccatgaat gtcgacaagt accggggcat tgtggttatg ggcacggtag 600
atctgggccc tctcgtcagg gccggatcca taccggaccg ttctcgtcagg gtggtcggac 660
atcgacgaca ccgcagctgc cgagacgacg ttgatacgtc caccggggcg gtccgtgatc 720
cacgccgtcg tcgccgttgc cgccactggc acgatgaggg ccatcaccga gaagacaacg 780
gccaccactc gcagaccacc tcgtcccaaa agagcgagga cgaaggcgat gacggcgatg 840
accagagccg gtacagccaa cgatcccacc agaacggagg agatgaaggt gagggcattg 900
tgtgagggga ggatcgcggc cactgaccac gccagtaccg gcagggtcag gatcagccc 960
acgagaccgg aagtgatgcg tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt 1020
ccaccgtact cacgggacat ggtcgatagg atcttcgcgc aggagggacc catggctatc 1080
aggatcagac aggttgctac cgaagacagg ccggccgtcg cgcgatgtc ccacggcgag 1140
tatgtttggc tggctgtcga caccgagtc gtcgttgatg gccttctcta ggtcttcgga 1200
ttgcctggg ccgggggtgca ccttgacgaa cctactccgc tggaactgga aagtctctac 1260

gtccgttctc	gtctgtacgg	caccgggctc	ggccaggccc	tcatgaatac	cgatcatcggc	1320
gattcccggg	cctatgtcat	ggtctatccc	gacaacaccc	aggccaaggc	attctaccgc	1380
cgtaacggat	tctctcccga	tgtcatctc	gacgattacc	gcgacgagga	tccggcctac	1440
gtcctggagt	gctggattcg	ctgaatcccc	ttggttcttg	ctcgcgacaa	gctaggataa	1500
attaaattta	tttatttctt	gtgtcgatgc	gccacgacga	cgtagtggga	ccggctcagg	1560
ggatgacgac	ccggtcccgg	gccgtgagtc	acgaaggagt	gccatgtcca	taacaccacg	1620
aaagtgcaag	gctgccgccc	ttgccacagc	gccggtggcc	gctgccctcg	gtgcttacgg	1680
atttcttaaa	ggggcgacga	agttctattc	cagccagggt	aacggaactc	ccgagcagta	1740
caagatgacc	cttcctgggt	acgacctcgt	cccggaagg	tcgccgcgct	tcaagcgctt	1800
cacccatgtg	gaggatctcg	acgccccctg	cgacgagggt	tggaaagcac	tctaccagct	1860
caacaccacg	accgcccggc	tctactcctt	cacttctctc	gagaagatgt	tccgactgtc	1920
ggtcgacaa	accttcatgg	tggaaacagg	ttggcaggcc	ccggactact	acaagcccgg	1980
tgacatgttc	tggtggagtt	acgccgggtt	cggtgccgag	gtcgcgcgca	tggtccccgg	2040
caagtatctg	gtgtgggttc	ctgacacccg	tgacggcacc	aggacaccgg	gcgcaagttt	2100
cctgctaccg	cctggaatgc	cgtggaaccg	ctggagttag	gtcatcgccc	tggaaacctt	2160
cgacagtggc	aaccggacgc	gcatctactc	ccggtggaac	atctcggcct	ccgaggagtc	2220
cagtccgata	tcgggtcttc	tcatggatct	ggtcatgatg	gacggcggcg	gcatggtgaa	2280
ccgtcggatg	ttccaagggc	tggagaaggc	tgccgtcgga	actgctcgca	agaacatcgt	2340
tcctgcgcgc	ctatcagcgg	ttcatgggca	agtcctacgg	cactgacgac	gacctgcagt	2400
accgcgttcc	gtaccgggag	atccgctggg	cccgcgactt	ccctcgagtg	gccagcgaac	2460
gggcctcctt	caccgaggat	cccaactggc	cgctcgcccc	gggggaggag	taccacgccg	2520
acatcgaagg	caacaatgcc	cgtaacgggt	ggaccgagga	caccccgggc	gtcaatgatg	2580
cccaggccga	gcggcggggc	aaggagctgg	cagcacatct	cgatgagatg	gcacgtggtc	2640
ggcgaactgc	ccgctgagat	gtttcgcgac	ctataccatt	accgacccca	ttcatcgccg	2700
aacttattca	ccactacatc	gacaagggaag	aacgatgtcc	atctcgaagg	attcacgtat	2760
cgccatcatc	ggggctggcc	cgcccgggct	ggctgccgga	atgtacctcg	aacaggccgg	2820
attcacgac	tacacgatcc	tggaaacgcac	cgaccacgtc	ggaggcaagt	gccactcacc	2880
gaactaccac	ggccgtcgtt	atgagatggg	ggccatcatg	ggcgccccca	gttacgacac	2940
catccaggag	atcatggatc	gcactggcga	caaggtcgac	gggccgaaac	tgcgctcgca	3000
gttctgcac	gaggacggcg	agatctacgt	ccggaaaaag	gatccagtgc	gtggtccgca	3060
ggtcatggca	gcagtgcaga	agctgggcca	gttgcctcg	acgaagtacc	agggatatga	3120
cgccaacggc	cactacaaca	aggttcacga	ggacctcatg	ctgcccttcg	acgagttcct	3180
cgccctcaac	gggtgcgagg	ccgcccgcga	cctgtggatc	aaccccttca	cggccttcgg	3240
ctacgggcac	ttcgacaacg	tcccggccgc	ctacgtgctg	aagtacctcg	acttcgtcac	3300
catgatgtcc	tttgccaagg	gagatctgtg	gacgtggggc	gacggcaccc	aggcgatgtt	3360
cgagcacctc	aacggcaccc	tggagcaccc	ggccgaacgc	aacggtgaca	tactcgcgat	3420
cacccgcgag	gacggcaagg	tccacattca	caccacggac	tgggatcgcg	agtcggacgt	3480
cctcgtcctc	accgtcccgc	tggaaaagtt	cctcgactac	tccgacgcgg	acgatgacga	3540
gcgggagtac	ttctcgaaga	tcatccacca	gcagtacatg	gtggatgcct	gcctggtgaa	3600
ggagtaccgg	accatctccg	ggtacgtccc	cgacaacatg	aggcccgaac	gtctcgggca	3660
cgatcatggt	tactaccacc	gctgggctga	tgatccgcac	cagatcatca	cgacctacct	3720
gctacgtaac	catccggact	acgcggacaa	gactcaggag	gagtgccgcc	agatggtcct	3780
cgacgacatg	gagaccttcg	gtcatccggg	cgagaagatc	atcgaggagc	agacctggta	3840
ctacttcccg	cacgttagct	cggaggacta	caaggccggg	tggtacgaga	aggtcgaggg	3900
aatgcagggt	cgctgcgaaca	ccttctacgc	cgagaaaatt	atgagtttcg	gtaatttcga	3960
cgagggtgtg	cactactcga	aggacctggt	gcgcgggttc	ttcggtgtgag	gtgtattccc	4020
gcattgctgc	ggggatgaga	atgggggggtg	gtaccgggtt	cggtaccacc	ccccatcgac	4080
cgtcgcgaac	cgggcctctg	tgaggcttcg	ggccggtagg	atcaggttat	ggatacttca	4140
gtcaatgtcg	acacgtcgtc	aagaccggcg	cacgaaccgg	ccaccgctcc	cggtcgtttc	4200
gtcgtcagag	atgcctgtca	cgaggacctg	cctgaagccg	cggtgttcca	ggcgtgtgac	4260
gtccgagaga	tccggccagg	ggtgatccct	aatgacgtcc	ttaccgaggt	cactggcccc	4320
ggtatcgtcc	acaccacat	tgagcagtg	aaccacttta	tggatgatgg	tgcatcttcc	4380
aagatccttg	ttgatcgctt	cgatatgagg	actgtcgggg	ttgccatggc	ccgggtctct	4440
acaagtcttg	atgctccccc	accgtgggag	atcgcgaccc	tccatgtact	gccagaggcg	4500
cgaaactgcg	gagcgtcaga	caacctcctc	gatgcttgta	tcgggaaccg	gtcggcctat	4560
gtgtgggtct	ttgccgataa	tgctcgcgcc	atttcgttct	accaacgcca	tgggttccac	4620
gtcgacgcgg	ccgacgggtg	cgttgacgat	tccctcggcg	gggtagagct	gcagcggctg	4680
atccgcgagg	acatcatcga	gtcgcagtg	tgatggatgg	gtagctcccg	tggctcgtcg	4740
gcatgccagc	acataggtct	agcgtgcctt	cagccgacga	tggtcctcac	acatgggacg	4800
agagcttggt	ggtgtcatcc	tgaatatgca	gggcgacttg	cttgagcttg	tcttcgtggg	4860
ctcgggcatg	gtgcgcgcag	aaaaggagct	cgccaccgtt	gcgcagcgtg	atgcgcacat	4920

```

aggcttgtgc gccgcaacga tcacaacggt ccgcagtggt aagggcttgg tgttcgatca 4980
tcgtgggtgct catgacaacc tcctccatct gaatcatcgg atcacctact agacaaccta 5040
cgctatcgtc ggaatgttct catacgtatc gaaagatgga tggctggggg cgaacacggt 5100
gccgggattc cgtgtcgtcg gctgtcgata agctgccacc gtgaccatgg acaacatctc 5160
gacctcatca gccaacagct cggaaacgcc acgtggtaag ggcgataccg tgcgcacggc 5220
gtcgactagc cgggagtacg gcgccaagaa tttattgggt ttggaggggc tcgag 5275

```

<210> 60
 <211> 1275
 <212> DNA
 <213> *Propionibacterium acnes*

<220>
 <221> CDS
 <222> (1)..(1272)

```

<400> 60
atg tcc atc tcg aag gat tca cgt atc gcc atc atc ggg gct ggc ccg 48
Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
1 5 10 15

gcc ggg ctg gct gcc gga atg tac ctc gaa cag gcc gga ttt cac gac 96
Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
20 25 30

tac acg atc ctg gaa cgc acc gac cac gtc gga ggc aag tgc cac tca 144
Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
35 40 45

ccg aac tac cac ggc cgt cgt tat gag atg ggg gcc atc atg ggc gtc 192
Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
50 55 60

ccc agt tac gac acc atc cag gag atc atg gat cgc act ggc gac aag 240
Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
65 70 75 80

gtc gac ggg ccg aaa ctg cgt cgc gag ttc ctg cac gag gac ggc gag 288
Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
85 90 95

atc tac gtc ccg gaa aag gat cca gtg cgt ggt ccg cag gtc atg gca 336
Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
100 105 110

gca gtg cag aag ctg ggc cag ttg ctc gcg acg aag tac cag gga tat 384
Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
115 120 125

gac gcc aac ggc cac tac aac aag gtt cac gag gac ctc atg ctg ccc 432
Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
130 135 140

ttc gac gag ttc ctc gcc ctc aac ggg tgc gag gcc gcc cga gac ctg 480
Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
145 150 155 160

tgg atc aac ccc ttc acg gcc ttc ggc tac ggg cac ttc gac aac gtc 528
Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val
165 170 175

```


ccg gcc gcc tac gtg ctg aag tac ctc gac ttc gtc acc atg atg tcc	576
Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser	
180 185 190	
ttt gcc aag gga gat ctg tgg acg tgg gcc gac ggc acc cag gcg atg	624
Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met	
195 200 205	
ttc gag cac ctc aac gcc acc ctg gag cac ccg gcc gaa cgc aac gtt	672
Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val	
210 215 220	
gac atc act cgc atc acc cgc gag gac ggc aag gtc cac att cac acc	720
Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr	
225 230 235 240	
acg gac tgg gat cgc gag tcc gac gtc ctc gtc ctc acc gtc ccg ctg	768
Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu	
245 250 255	
gaa aag ttc ctc gac tac tcc gac gcg gac gat gac gag cgg gag tac	816
Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr	
260 265 270	
ttc tcg aag atc atc cac cag cag tac atg gtg gat gcc tgc ctg gtg	864
Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val	
275 280 285	
aag gag tac ccg acc atc tcc ggg tac gtc ccc gac aac atg agg ccc	912
Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro	
290 295 300	
gaa cgt ctc ggg cac gtc atg gtt tac tac cac cgc tgg gct gat gat	960
Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp	
305 310 315 320	
ccg cac cag atc atc acg acc tac ctg cta cgt aac cat ccg gac tac	1008
Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr	
325 330 335	
gcg gac aag act cag gag gag tgc cgc cag atg gtc ctc gac gac atg	1056
Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met	
340 345 350	
gag acc ttc ggt cat ccg gtc gag aag atc atc gag gag cag acc tgg	1104
Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp	
355 360 365	
tac tac ttc ccg cac gtt agc tcg gag gac tac aag gcc ggg tgg tac	1152
Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr	
370 375 380	
gag aag gtc gag gga atg cag ggt cgt cgc aac acc ttc tac gcc gga	1200
Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly	
385 390 395 400	
gaa att atg agt ttc ggt aat ttc gac gag gtg tgc cac tac tcg aag	1248
Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys	
405 410 415	

gac ctg gtg acg cgg ttc ttc gtg tga
 Asp Leu Val Thr Arg Phe Phe Val
 420

1275

<210> 61
 <211> 424
 <212> PRT
 <213> Propionibacterium acnes

<400> 61

Met Ser Ile Ser Lys Asp Ser Arg Ile Ala Ile Ile Gly Ala Gly Pro
 1 5 10 15
 Ala Gly Leu Ala Ala Gly Met Tyr Leu Glu Gln Ala Gly Phe His Asp
 20 25 30
 Tyr Thr Ile Leu Glu Arg Thr Asp His Val Gly Gly Lys Cys His Ser
 35 40 45
 Pro Asn Tyr His Gly Arg Arg Tyr Glu Met Gly Ala Ile Met Gly Val
 50 55 60
 Pro Ser Tyr Asp Thr Ile Gln Glu Ile Met Asp Arg Thr Gly Asp Lys
 65 70 75 80
 Val Asp Gly Pro Lys Leu Arg Arg Glu Phe Leu His Glu Asp Gly Glu
 85 90 95
 Ile Tyr Val Pro Glu Lys Asp Pro Val Arg Gly Pro Gln Val Met Ala
 100 105 110
 Ala Val Gln Lys Leu Gly Gln Leu Leu Ala Thr Lys Tyr Gln Gly Tyr
 115 120 125
 Asp Ala Asn Gly His Tyr Asn Lys Val His Glu Asp Leu Met Leu Pro
 130 135 140
 Phe Asp Glu Phe Leu Ala Leu Asn Gly Cys Glu Ala Ala Arg Asp Leu
 145 150 155 160
 Trp Ile Asn Pro Phe Thr Ala Phe Gly Tyr Gly His Phe Asp Asn Val
 165 170 175
 Pro Ala Ala Tyr Val Leu Lys Tyr Leu Asp Phe Val Thr Met Met Ser
 180 185 190
 Phe Ala Lys Gly Asp Leu Trp Thr Trp Ala Asp Gly Thr Gln Ala Met
 195 200 205
 Phe Glu His Leu Asn Ala Thr Leu Glu His Pro Ala Glu Arg Asn Val
 210 215 220
 Asp Ile Thr Arg Ile Thr Arg Glu Asp Gly Lys Val His Ile His Thr
 225 230 235 240
 Thr Asp Trp Asp Arg Glu Ser Asp Val Leu Val Leu Thr Val Pro Leu
 245 250 255
 Glu Lys Phe Leu Asp Tyr Ser Asp Ala Asp Asp Asp Glu Arg Glu Tyr
 260 265 270

Phe Ser Lys Ile Ile His Gln Gln Tyr Met Val Asp Ala Cys Leu Val
 275 280 285
 Lys Glu Tyr Pro Thr Ile Ser Gly Tyr Val Pro Asp Asn Met Arg Pro
 290 295 300
 Glu Arg Leu Gly His Val Met Val Tyr Tyr His Arg Trp Ala Asp Asp
 305 310 315 320
 Pro His Gln Ile Ile Thr Thr Tyr Leu Leu Arg Asn His Pro Asp Tyr
 325 330 335
 Ala Asp Lys Thr Gln Glu Glu Cys Arg Gln Met Val Leu Asp Asp Met
 340 345 350
 Glu Thr Phe Gly His Pro Val Glu Lys Ile Ile Glu Glu Gln Thr Trp
 355 360 365
 Tyr Tyr Phe Pro His Val Ser Ser Glu Asp Tyr Lys Ala Gly Trp Tyr
 370 375 380
 Glu Lys Val Glu Gly Met Gln Gly Arg Arg Asn Thr Phe Tyr Ala Gly
 385 390 395 400
 Glu Ile Met Ser Phe Gly Asn Phe Asp Glu Val Cys His Tyr Ser Lys
 405 410 415
 Asp Leu Val Thr Arg Phe Phe Val
 420

<210> 62
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> RBS
 <222> (1)..(7)
 <400> 62
 aaggaag

7

<210> 63
 <211> 1073
 <212> DNA
 <213> Propionibacterium acnes

<400> 63
 gccgggagg caccattgac gaatttcgc acactggatg gcggaacaaa ggtgtcgtga 60
 tttccctgga tcaccattgt tgggtggtgcc tgaggagtga tccaggtgga actgttgaca 120
 gcgcgataac ggtcggggaa ttgcttgggg gtgccaccga tatacatttt ggccggcattg 180
 cccgcgtca gtgtggtgac cgactcgacg gtaccgacat ccaccgttgg atagagggcg 240
 aggactgact tcggggcccg tattgagccg caggaactct tcaactttcc actggcggcg 300
 ccgtaggcga gattaatggc cattccacca ccagcgggaat caccatgat cgatacctgt 360
 gaagggtcgc caccgagttc ttccacgtgg gacaggctcc agggccaggc acatgcgacc 420
 tgttttgggg cggtattcca ggtgggggtg ccctgggtgg ccaggggtga cgaggggcga 480
 atgactaacc agccatgatc ggaaaacat ctcaacgtgg cgggcattgt ggcgtcgggtg 540

ctccatcctt caccatgaat gtcgacaagt accggggcat tgtggttatg ggcacggtag 600
atctgggccc tctcgtcagg gccggatcca taccggaccg tttcgtcagg gtggtcggac 660
atcgacgaca ccgcagctgc cgagacgacg ttgatacgtc caccggggcg gtccgtgatc 720
cacgccgtcg tcgccgttgc cgccactggc acgatgaggg ccatcaccca gaagacaacg 780
gccaccactc gcagaccacc tcgtcccaaa agagcgagga cgaaggcgat gacggcgatg 840
accagagccg gtacagccaa cgatccacc agaacggagg agatgaaggt gaggggcattg 900
tgtgagggga ggatcgcggc cactgaccac gccagtaccg gcagggtcag gatcagccccg 960
acgagaccgg aagtgatgcg tagccaggaa tgacgggagg ttttcgtgtc agccacgcgt 1020
ccaccgtact cacgggacat ggtcgatagg atcttcgcgc aggagggacc cat 1073

<210> 64
<211> 358
<212> PRT
<213> Propionibacterium acnes

<400> 64
Met Gly Pro Ser Cys Ala Lys Ile Leu Ser Thr Met Ser Arg Glu Tyr
1 5 10 15
Gly Gly Arg Val Ala Asp Thr Lys Thr Ser Arg His Ser Trp Leu Arg
20 25 30
Ile Thr Ser Gly Leu Val Gly Leu Ile Leu Thr Leu Pro Val Leu Ala
35 40 45
Trp Ser Val Ala Ala Ile Leu Pro Ser His Asn Ala Leu Thr Phe Ile
50 55 60
Ser Ser Val Leu Val Gly Ser Leu Ala Val Pro Ala Leu Val Ile Ala
65 70 75 80
Val Ile Ala Phe Val Leu Ala Leu Leu Gly Arg Gly Gly Leu Arg Val
85 90 95
Val Ala Val Val Phe Ser Val Met Ala Leu Ile Val Pro Val Ala Ala
100 105 110
Thr Ala Thr Thr Ala Trp Ile Thr Asp Arg Pro Gly Gly Arg Ile Asn
115 120 125
Val Val Ser Ala Ala Ala Val Ser Ser Met Ser Asp His Pro Asp Glu
130 135 140
Thr Val Arg Tyr Gly Ser Gly Pro Asp Glu Thr Ala Gln Ile Tyr Arg
145 150 155 160
Ala His Asn His Asn Ala Pro Val Leu Val Asp Ile His Gly Glu Gly
165 170 175
Trp Ser Thr Asp Ala Thr Met Pro Ala Thr Leu Arg Trp Phe Ser Asp
180 185 190
His Gly Trp Leu Val Ile Arg Pro Ser Tyr Thr Leu Ala Thr Gln Gly
195 200 205
His Pro Thr Trp Asn Thr Ala Pro Lys Gln Val Ala Cys Ala Trp Ala
210 215 220
Trp Ser Leu Ser His Val Lys Glu Leu Gly Gly Asp Pro Ser Gln Val
225 230 235 240

Ser Ile Met Gly Asp Ser Ala Gly Gly Gly Met Ala Ile Asn Leu Ala
 245 250 255
 Tyr Gly Ala Ala Ser Gly Lys Leu Lys Ser Ser Cys Gly Ser Ile Arg
 260 265 270
 Ala Pro Lys Ser Val Leu Ala Leu Tyr Pro Thr Val Asp Val Gly Thr
 275 280 285
 Val Glu Ser Val Thr Thr Leu Ser Ala Gly Asn Ala Ala Lys Met Tyr
 290 295 300
 Ile Gly Gly Thr Pro Lys Gln Phe Pro Asp Arg Tyr Arg Ala Val Asn
 305 310 315 320
 Ser Ser Thr Trp Ile Thr Pro Gln Ala Pro Pro Thr Met Val Ile Gln
 325 330 335
 Gly Asn His Asp Thr Phe Val Pro Pro Ser Ser Val Arg Lys Phe Val
 340 345 350
 Asn Arg Ala Arg Pro Ala
 355

<210> 65
 <211> 783
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1)..(783)

<400> 65
 atg tcc ata aca cca cga aag tgc aag gct gcc gcc ctt gcc aca gcg 48
 Met Ser Ile Thr Pro Arg Lys Cys Lys Ala Ala Ala Leu Ala Thr Ala
 1 5 10 15
 ccg gtg gcc gct gcc ctc ggt gct tac gga ttt ctt aaa ggg gcg acg 96
 Pro Val Ala Ala Ala Leu Gly Ala Tyr Gly Phe Leu Lys Gly Ala Thr
 20 25 30
 aag ttc tat tcc agc cag gtt aac gga act ccc gag cag tac aag atg 144
 Lys Phe Tyr Ser Ser Gln Val Asn Gly Thr Pro Glu Gln Tyr Lys Met
 35 40 45
 acc ctt cct ggt gac gac ctc gtc ccg gaa ggt tcg ccg cgc ttc aag 192
 Thr Leu Pro Gly Asp Asp Leu Val Pro Glu Gly Ser Pro Arg Phe Lys
 50 55 60
 cgc ctc acc cat gtg gag gat ctc gac gcc ccc tgc gac gag gtc tgg 240
 Arg Leu Thr His Val Glu Asp Leu Asp Ala Pro Cys Asp Glu Val Trp
 65 70 75 80
 aag cac gtc tac cag ctc aac acc acg acc gcc ggc ttc tac tcc ttc 288
 Lys His Val Tyr Gln Leu Asn Thr Thr Thr Ala Gly Phe Tyr Ser Phe
 85 90 95
 acc ttc ttc gag aag atg ttc gga ctg tcg gtc gac aac acc ttc atg 336

Thr	Phe	Phe	Glu	Lys	Met	Phe	Gly	Leu	Ser	Val	Asp	Asn	Thr	Phe	Met		
			100					105					110				
gtg	gaa	cag	gct	tgg	cag	gcc	ccg	gac	tac	tac	aag	ccc	ggg	gac	atg	384	
Val	Glu	Gln	Ala	Trp	Gln	Ala	Pro	Asp	Tyr	Tyr	Lys	Pro	Gly	Asp	Met		
		115					120					125					
ttc	tgt	tgg	agt	tac	gcc	ggg	ttc	ggg	gcc	gag	gtc	gcc	gac	atg	gtc	432	
Phe	Cys	Trp	Ser	Tyr	Ala	Gly	Phe	Gly	Ala	Glu	Val	Ala	Asp	Met	Val		
	130					135					140						
ccc	ggc	aag	tat	ctg	gtg	tgg	ttc	gct	gac	acc	cgt	gac	ggc	acc	agg	480	
Pro	Gly	Lys	Tyr	Leu	Val	Trp	Phe	Ala	Asp	Thr	Arg	Asp	Gly	Thr	Arg		
145					150					155					160		
aca	ccg	ggc	gca	agt	ttc	ctg	cta	ccg	cct	gga	atg	ccg	tgg	aac	cgc	528	
Thr	Pro	Gly	Ala	Ser	Phe	Leu	Leu	Pro	Pro	Gly	Met	Pro	Trp	Asn	Arg		
				165					170					175			
tgg	agt	tgg	gtc	atc	gcc	ctg	gaa	ccc	ctc	gac	agt	ggc	aac	cgg	acg	576	
Trp	Ser	Trp	Val	Ile	Ala	Leu	Glu	Pro	Leu	Asp	Ser	Gly	Asn	Arg	Thr		
			180					185					190				
cgc	atc	tac	tcc	cgg	tgg	aac	atc	tcg	gcc	tcc	gag	gag	tcc	agt	ccg	624	
Arg	Ile	Tyr	Ser	Arg	Trp	Asn	Ile	Ser	Ala	Ser	Glu	Glu	Ser	Ser	Pro		
		195				200						205					
atc	tcg	gtc	ttc	ctc	atg	gat	ctg	gtc	atg	atg	gac	ggc	ggc	ggc	atg	672	
Ile	Ser	Val	Phe	Leu	Met	Asp	Leu	Val	Met	Met	Asp	Gly	Gly	Gly	Met		
		210				215					220						
gtg	aac	cgt	cgg	atg	ttc	caa	ggg	ctg	gag	aag	gct	gcc	gtc	gga	act	720	
Val	Asn	Arg	Arg	Met	Phe	Gln	Gly	Leu	Glu	Lys	Ala	Ala	Val	Gly	Thr		
225					230					235					240		
gct	cgc	aag	aac	atc	gtt	cct	gcg	cgc	cta	tca	gcg	gtt	cat	ggg	caa	768	
Ala	Arg	Lys	Asn	Ile	Val	Pro	Ala	Arg	Leu	Ser	Ala	Val	His	Gly	Gln		
				245					250					255			
gtc	eta	cgg	cac	tga												783	
Val	Leu	Arg	His														
			260														

<210> 66

<211> 260

<212> PRT

<213> Propionibacterium acnes

<400> 66

Met	Ser	Ile	Thr	Pro	Arg	Lys	Cys	Lys	Ala	Ala	Ala	Leu	Ala	Thr	Ala		
1				5					10					15			
Pro	Val	Ala	Ala	Ala	Leu	Gly	Ala	Tyr	Gly	Phe	Leu	Lys	Gly	Ala	Thr		
		20						25					30				
Lys	Phe	Tyr	Ser	Ser	Gln	Val	Asn	Gly	Thr	Pro	Glu	Gln	Tyr	Lys	Met		
		35					40					45					
Thr	Leu	Pro	Gly	Asp	Asp	Leu	Val	Pro	Glu	Gly	Ser	Pro	Arg	Phe	Lys		
	50					55					60						
Arg	Leu	Thr	His	Val	Glu	Asp	Leu	Asp	Ala	Pro	Cys	Asp	Glu	Val	Trp		
	65				70					75					80		
Lys	His	Val	Tyr	Gln	Leu	Asn	Thr	Thr	Thr	Ala	Gly	Phe	Tyr	Ser	Phe		

Thr	Phe	Phe	Glu	85	Lys	Met	Phe	Gly	Leu	90	Ser	Val	Asp	Asn	Thr	95	Phe	Met
			100						105							110		
Val	Glu	Gln	Ala	Trp	Gln	Ala	Pro	Asp	Tyr	Tyr	Lys	Pro	Gly	Asp	Met			
		115						120					125					
Phe	Cys	Trp	Ser	Tyr	Ala	Gly	Phe	Gly	Ala	Glu	Val	Ala	Asp	Met	Val			
	130					135					140							
Pro	Gly	Lys	Tyr	Leu	Val	Trp	Phe	Ala	Asp	Thr	Arg	Asp	Gly	Thr	Arg			
	145				150					155					160			
Thr	Pro	Gly	Ala	Ser	Phe	Leu	Leu	Pro	Pro	Gly	Met	Pro	Trp	Asn	Arg			
				165					170					175				
Trp	Ser	Trp	Val	Ile	Ala	Leu	Glu	Pro	Leu	Asp	Ser	Gly	Asn	Arg	Thr			
		180						185					190					
Arg	Ile	Tyr	Ser	Arg	Trp	Asn	Ile	Ser	Ala	Ser	Glu	Glu	Ser	Ser	Pro			
	195					200						205						
Ile	Ser	Val	Phe	Leu	Met	Asp	Leu	Val	Met	Met	Asp	Gly	Gly	Gly	Met			
	210				215						220							
Val	Asn	Arg	Arg	Met	Phe	Gln	Gly	Leu	Glu	Lys	Ala	Ala	Val	Gly	Thr			
	225				230					235					240			
Ala	Arg	Lys	Asn	Ile	Val	Pro	Ala	Arg	Leu	Ser	Ala	Val	His	Gly	Gln			
			245						250					255				
Val	Leu	Arg	His															
			260															

<210> 67
 <211> 7
 <212> DNA
 <213> Propionibacterium acnes

BEST AVAILABLE COPY

<220>
 <221> RBS
 <222> (1)..(7)

<400> 67
 gaaggag

7

<210> 68
 <211> 582
 <212> DNA
 <213> Propionibacterium acnes

<220>
 <221> CDS
 <222> (1)..(582)

<400> 68																		
atg	gat	act	tca	gtc	aat	gtc	gac	acg	tcg	tca	aga	ccg	gcg	cac	gaa			48
Met	Asp	Thr	Ser	Val	Asn	Val	Asp	Thr	Ser	Ser	Arg	Pro	Ala	His	Glu			
1				5				10					15					
ccg	gcc	acc	gct	ccc	ggt	cgt	ttc	gtc	gtc	aga	gat	gcc	tgt	cac	gag			96
Pro	Ala	Thr	Ala	Pro	Gly	Arg	Phe	Val	Val	Arg	Asp	Ala	Cys	His	Glu			
			20					25					30					
gac	ctg	cct	gaa	gcc	gcg	gct	gtt	cag	gcc	gtg	tgc	gtc	cga	gag	atc			144
Asp	Leu	Pro	Glu	Ala	Ala	Ala	Val	Gln	Ala	Val	Cys	Val	Arg	Glu	Ile			
			35				40					45						

ggc cag ggg gtg atc cct aat gag gtc ctt acc gag gtc act ggc ccc	192
Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro	
50 55 60	
ggt atc gtc cac acc acc att gag cag tgg aac cac ttt atg gat gat	240
Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp	
65 70 75 80	
ggt gcg atc ttc aag atc ctt gtt gat cgc ctc gat atg agg act gtc	288
Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val	
85 90 95	
ggg gtt gcc atg gcc cgg gtc tct aca agt tct gat gct ccc aca ccg	336
Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro	
100 105 110	
tgg gag atc gcg acc ctc cat gta ctg cca gag gcg cga aac tgc gga	384
Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly	
115 120 125	
gcg tca gac aac ctc ctc gat gct tgt atc ggg aac cgg tcg gcc tat	432
Ala Ser Asp Asn Leu Leu Asp Ala Cys Ile Gly Asn Arg Ser Ala Tyr	
130 135 140	
gtg tgg gtc ttt gcc gat aat gct cgc gcc att tcg ttc tac caa cgc	480
Val Trp Val Phe Ala Asp Asn Ala Arg Ala Ile Ser Phe Tyr Gln Arg	
145 150 155 160	
cat ggg ttc cac gtc gac gcg gcc gac ggt gcc gtt gac gat tcc ctc	528
His Gly Phe His Val Asp Ala Ala Asp Gly Ala Val Asp Asp Ser Leu	
165 170 175	
ggc ggg gta gag ctg cag cgg ctg atc cgc gag gac atc atc gag tcg	576
Gly Gly Val Glu Leu Gln Arg Leu Ile Arg Glu Asp Ile Ile Glu Ser	
180 185 190	
cag tga	582
Gln	

<210> 69

<211> 193

<212> PRT

<213> Propionibacterium acnes

<400> 69

Met Asp Thr Ser Val Asn Val Asp Thr Ser Ser Arg Pro Ala His Glu	
1 5 10 15	
Pro Ala Thr Ala Pro Gly Arg Phe Val Val Arg Asp Ala Cys His Glu	
20 25 30	
Asp Leu Pro Glu Ala Ala Ala Val Gln Ala Val Cys Val Arg Glu Ile	
35 40 45	
Gly Gln Gly Val Ile Pro Asn Asp Val Leu Thr Glu Val Thr Gly Pro	
50 55 60	
Gly Ile Val His Thr Thr Ile Glu Gln Trp Asn His Phe Met Asp Asp	
65 70 75 80	
Gly Ala Ile Phe Lys Ile Leu Val Asp Arg Leu Asp Met Arg Thr Val	
85 90 95	
Gly Val Ala Met Ala Arg Val Ser Thr Ser Ser Asp Ala Pro Thr Pro	
100 105 110	
Trp Glu Ile Ala Thr Leu His Val Leu Pro Glu Ala Arg Asn Cys Gly	

<223> Xaa = any amino acid

<400> 73

Gly Xaa Gly Xaa Xaa Gly Xaa Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Glu Xaa Xaa Xaa
20 25 30
Xaa Xaa Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
35 40 45
Xaa Xaa Xaa Xaa Gly
50

<210> 74

<211> 43

<212> PRT

<213> Homo sapiens

<400> 74

Ser Glu Ala Tyr Ser Ala Lys Ile Ala Leu Phe Gly Ala Gly Pro Ala
1 5 10 15
Ser Ile Ser Cys Ala Ser Phe Leu Ala Arg Leu Gly Tyr Ser Asp Ile
20 25 30
Thr Ile Phe Glu Lys Gln Glu Tyr Val Gly Gly
35 40

<210> 75

<211> 41

<212> PRT

<213> Agrobacterium vitis

<400> 75

Lys Val Ala Ile Val Gly Ala Gly Leu Ser Gly Leu Val Val Ala Ser
1 5 10 15
Glu Leu Leu His Ala Gly Ile Asp Asp Val Thr Leu Tyr Glu Ala Ser
20 25 30
Asp Arg Ile Gly Gly Lys Leu Trp Ser
35 40

<210> 76

<211> 45

<212> PRT

<213> Deinococcus radiodurans

<400> 76

Val Lys Thr Gly Lys Lys Val Ala Val Val Gly Ser Gly Pro Ala Gly
1 5 10 15
Leu Ala Ala Ala Gln Gln Leu Ala Arg Ala Gly His Asp Val Thr Val
20 25 30
Phe Glu Lys Asn Asp Arg Val Gly Gly Arg Ile Glu Gln

35

40

45

<210> 77

<211> 37

<212> PRT

<213> *Arthrobacter nicotinovorans*

<400> 77

Val Val Gly Gly Gly Phe Ser Gly Leu Lys Ala Ala Arg Asp Leu Thr
 1 5 10 15

Asn Ala Gly Lys Lys Val Leu Leu Leu Glu Gly Gly Glu Arg Leu Gly
 20 25 30

Gly Arg Ala Tyr Ser
 35

<210> 78

<211> 52

<212> PRT

<213> *Synechocystis* sp.

<400> 78

Arg Ile Ala Ile Ile Gly Ala Gly Leu Ala Gly Met Ala Thr Ala Val
 1 5 10 15

Glu Leu Val Asp Ala Gly His Glu Val Glu Leu Tyr Glu Ala Arg Ser
 20 25 30

Phe Ile Gly Gly Lys Val Gly Ser Trp Val Asp Gly Asp Gly Asn His
 35 40 45

Ile Glu Met Gly
 50

<210> 79

<211> 57

<212> PRT

<213> *Cercospora nicotianae*

<400> 79

Ser Thr Ser Lys Arg Pro Thr Ala Ile Val Ile Gly Ser Gly Val Gly
 1 5 10 15

Gly Val Ser Thr Ala Ala Arg Leu Ala Arg Ala Gly Phe His Val Thr
 20 25 30

Val Leu Glu Lys Asn Asn Phe Thr Gly Gly Arg Cys Ser Leu Ile His
 35 40 45

His Glu Gly Tyr Arg Phe Asp Gln Gly
 50 55

<210> 80

<211> 52

<212> PRT

<213> *Zea mays*

<400> 80

Arg Val Ile Val Val Gly Ala Gly Met Ser Gly Ile Ser Ala Ala Lys
1 5 10 15

Arg Leu Ser Glu Ala Gly Ile Thr Asp Leu Leu Ile Leu Glu Ala Thr
20 25 30

Asp His Ile Gly Gly Arg Met His Lys Thr Asn Phe Ala Gly Ile Asn
35 40 45

Val Glu Leu Gly
50

BEST AVAILABLE COPY